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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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e 680, App e 6, App e 72, App e 95, App e 35,		, , Ab Ab A	340, A 358, A 358, A 39, A 1165, A 1163, A 1165, A 1165, A 11349, 2720, A 2720, A 2720, A 2720, A	e 108, e 17449, e 735, e 734, e 735, e 849, e 849,	Description Sequence 2, Appli Sequence 538, App Sequence 538, App Sequence 538, App Sequence 538, App

ALIGNMENTS

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Sequence 2, Application US/09292437

GENERAL INFORMATION:
APPLICANT: Olaf Schneewind
APPLICANT: Sarkis Mazmanian
APPLICANT: Hung Ton-That
APPLICANT: Hung Ton-That
TITLE OF INVENTION: IDENTIFICATION OF SORTA
FILE REFERENCE: 510015 213
CURRENT APPLICATION NUMBER: US/09/292,437
CURRENT APPLICATION NUMBER: US/09/292,437
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 621
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-09-292-437-2
RESULT 2
US-08-781-986A-538/c
; Sequence 538, Application US/08781986A
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Best Local Similarity 100.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US
FILING DATE:
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MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Benson, Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STRANDEDNESS: double
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COMPUTER: HE
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                gtaagctttgcagaagaaatgaatcactagatgatcaaaatatttcaattgcaggacac
                                                            actttcattgaccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagt
                                                                                                                                                                      gctgatattaaagaaccagtatatccaggaccagcaacacctgaacaattaaatagaggt
                                                                                                                                                                                                                             gctaaacctcaaattccgaaagataaatcgaaagtggcaggctatattgaaattccagat
                                                                                                                                                                                                                                                                    aagattgaacaatatgataaaatgtaaaaagaacaggcgagtaaagataaaaagcagcaa 180
                                            ACTTTCATTGACCGTCCGAACTATCAATTTACAAATCTTAAAGCAGCCAAAAAAAGGTAGT
                                                                                                   GTAAGCTTTGCAGAAGAAAATGAATCACTAGATGATCAAAATATTTCAATTGCAGGACAC
                                                                                                                                                          GCTGATATTAAAGAACCAGTATATCCAGGACCAGCAACACCTGAACAATTAAATAGAGGT
                                                                                                                                                                                                                GCTAAACCTCAAATTCCGAAAGATAAATCGAAAGTGGCAGGCTATATTGAAATTCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301) 309-8504
(301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HP Vectra
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5255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PB248PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 621; DB 11;
Pred. No. 1.2e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                   371
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Вb

310

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US-08-956-171-538/c
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              В
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                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 538:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 538, Application US/08956171
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                        730
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               610
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OPERATING SYSTEM:
SOFTWARE: ASCII T
                                                                                             61
                                                                                                                                                                                                                                                                         TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Benson, Bob
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                gtagctacagaagtcaaataa 621
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                            aagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaa 180
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              AAGATTGAACAATATGATAAAAATGTAAAAGAACAGGCGAGTAAAGATAAAAAGCAGCAA
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                                                                                                                                                                                                                                                                            double
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                                                                                                                                                                                        100.0%; Score 621; DB 13; 100.0%; Pred. No. 1.2e-106;
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5255
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                                                                                                                                                                                                    Length 3733;
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                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171B
          TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 610-5790
                                                                            APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and NUMBER OF SEQUENCES: 5255
                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gctaaacctcaaattccgaaagataaatcgaaagtggcaggctatattgaaattccagat
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                                                                                                                                                                                                                                                                                       ZIP:
                                   NAME: HOOVER, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                             FILING DATE: 20-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                  OPERATING
                                                                                                                                                                                                                                                COMPUTER:
TELEFAX: (301)
                                                                   NAME:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human
                                                                                                                                                                                                                                                                                         20850
                                                                                                                                                                                                                                                                                                                                                                                                                Steven C. Barash
Michael R. Fannon
                                                                                                                                                                                                                                                                                                                                                                                                                                           Patrick S. Dillon
Craig A. Rosen
                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                  SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi
                                                                                                                                                                                                                                                                                                                                                         Genome Sciences,
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US-08-827-356-2678; Sequence 2678, Application US/08827356; GENERAL INFORMATION:
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US-08-956-171B-538
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 538:
SEQUENCE CHARACTERISTICS:
LENGTH: 3733 base pairs
                                     APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: STAPHYLOCOCCUS
TITLE OF INVENTION: COMPOSITIONS AN
NUMBER OF SEQUENCES: 5574
                                                                                                           APPLICANT:
                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       481
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                  ADDRESSEE:
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nes 621; Conserv
                                                                                                                                                                                                                                                                                                                                                                               TTAATTACTTGTGATGATTACAATGAAAAGACAGGCGTTTGGGAAAAAACGTAAAATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTTTCATTGACCGTCCGAACTATCAATTTACAAATCTTAAAGCAGCCAAAAAAAGGTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
    2000
                                                                                           George H. Shimer, Jr. George H. Miller Roberta S. Hare
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 Schering-Plough Corporation 00 Galloping Hill Road
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Pred. No. 1.2e-106;
Pred. No. 1.2e-106;
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                                                         AND
                                                                     AUREUS RELATED
                                                       METHODS
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Best Local Similarity
Matches 615; Conserv
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FILING DATE: 14-JUN-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New Jerse, STATE: New Jerse, COUNTRY: USA COUNTRY: 07033-0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM.PC compati
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                             424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM.PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                      64
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gttaagcctacagatgtaggagttctagatgaacaaaaaggtaaagataaacaattaaca
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/01:
FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/01:
FILING DATE: 02-MAY-1996
ADDITATION NUMBER: 60/010 atggtgtactttaaagttggtaatgaaacacgtaagtataaaatgacaagtataagagat 480 gctgatattaaagaaccagtatatccaggaccagcaacacctgaacaattaaatagaggt 300 gctaaacctcaaattccgaaagataaatcgaaagtggcaggctatattgaaattccagat 240 GCTGATATTAAAGAACCAGTATATCCAGGACCAGCAACACCTGAACAATTAAATAGAGGT 303 GCTAAACCTCAAATTCCGAAAGATAAATCAAAAGTGGCAGGCTATATTGAAATTCCAGAT 243 AAGATTGAACAATATGATAAAAATGTAAAAGAACAGGCGAGTAAAGACAATAAGCAGCAA 183 aagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaa 180 GTAAGCTTTGCAGAAAATGAATCACTAGATGATCAAAATATTTCAATTGCAGGACAC Staphylococcus DNA (genomic) PC-DOS/MS-DOS 98.5%; 99.0%; 60/016,743 60/020,016 60/014,477 US/08/827,356 Score 611.4; DB 12; Pred. No. 6.1e-105; 0; Mismatches 6; aureus DB 12; Length

624; 0;

Gaps

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CURRENT APPLICATION NUMBER: US/09/611,529
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/253,718
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
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US-09-611-529-2938
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Karen J. Shaw
TITLE OF INVENTION: Staphylococcus aureus
FILE REFERENCE: 1034/10963US1
EQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR FILING DATE: 1996-04-01
OR APPLICATION NUMBER: US 60
OR FILING DATE: 1996-05-02
OR APPLICATION NUMBER: US 60
OR FILING DATE: 1996-06-14
                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/035,079
FILING DATE: 1998-03-06
APPLICATION NUMBER: US 09/035,079
APPLICATION NUMBER: US 09/035,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/266,541
FILING DATE: 199-03-11
APPLICATION NUMBER: US 09/037,934
FILING DATE: 1998-03-10
APPLICATION NUMBER: US 09/036,720
FILING DATE: 1998-03-06
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APPLICATION NUMBER: US 09/036.137
FILING DATE: US 09/036.137
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APPLICATION NUMBER:
FILING DATE: 1998-(
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FILING DATE: 1998-03-06

FILING DATE: 1707
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NO 2938
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George H. Miller
Roberta S. Hare
                             SON
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1998-03-06
NUMBER:
                                                                                                                                          1997-04-01
UMBER: US 08/831,156
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1998-03-06
MBER
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UMBER: US 09/036,081
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US-08-831-156A-108
; Sequence 108, Application US/08831156A
; GENERAL INFORMATION:
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Best Local Similarity 99.0%;
Matches 615; Conservative
                                                                              APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: GENOME AND RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHO
NUMBER OF SEQUENCES: 112
                                                                CORRESPONDENCE ADDRESS:
                       STREET:
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                        Kenilworth
          New Jersey
                                      2000 Galloping
                                    Schering-Plough (
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; Pred. No. 6.1e
0; Mismatches
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                                    Corporation
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

MEDIUM TYPE:

READABLE FORM: TYPE: Floppy disk

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Best Local Similarity
Matches 615; Conserv
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LOCATION: 1...91077
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                                                             15581
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FILING DATE: 01-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,477
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LENGTH: 91077 base pai
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FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/016,743
FILING DATE: 02-MAY-1996
APPLICATION NUMBER: 60/020,016
FILING DATE: 14-JUN-1996
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TYPE: nucleic acid
STRANDEDNESS: double
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              gttaagcctacagatgtaggagttctagatgaacaaaaaggtaaagataaacaattaaca
                                                                                                                                                                                                                                                                                                                   gcatatttgtttgctaaaccacatatcgataattatcttcacgataaagataaagatgaa 120
                                                                                                                                                                                         GTAAGCTTTGCAGAAGAAATGAATCACTAGATGATCAAAATATTTCAATTGCAGGACAC
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GTTAAGCCAACAGATGTAGAAGTTCTAGATGAACAAAAAGGTAAAGATAAACAATTAACA
                                                             ATGGTGTACTTTAAAGTTGGTAATGAAACACGTAAGTATAAAATGACAAGTATAAGAGAT
                                                                        atggtgtactttaaagttggtaatgaaacacgtaagtataaaatgacaagtataagagat
                                                                                                                          ACTTTCATTGACCGTCCGAACTATCAATTTACAAATCTTAAAGCAGCCAAAAAAAGGTAGT
                                                                                                                                          actttcattgaccgtccgaactatcaatttacaaatcttaaagcagccaaaaaaggtagt
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                                                                                                                                                                                                                                                       GCTGATATTAAAGAACCAGTATATCCAGGACCAGCAACACCTGAACAATTAAATAGAGGT
                                                                                                                                                                                                                                                                      gctgatattaaagaaccagtatatccaggaccagcaacacctgaacaattaaatagaggt 300
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Pred. No. 1.
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; ORGANISM: Staphylococcus aureus US-09-611-529-7449
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                                                            SEQ ID NO 7449
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                                                                      PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1996-06-14 NUMBER OF SEQ ID NOS: 7451
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CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/353,718
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR APPLICATION NUMBER: US 09/266,557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                            LENGTH:
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R FILING DATE: 1998-03
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FILING DATE: 1999-03-11
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FILING DATE: 1996-04-01
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FILING DATE: 1997-04-01
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                                              812842
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UMBER: US 09/266,541
1999-03-11
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JMBER: US 09/036,079
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1998-03-06
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JMBER: US 09/036,720
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                                                                                                                                           Sequence 735, Application US/60038697

GENERAL INFORMATION:
APPLICANT: Lagace, Robert E.
APPLICANT: Corley, Neil C.
APPLICANT: RUSSO, Frank D.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STAPHLOCOCCUS AUREUS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1027
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Best Local Similarity
Matches 615; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for 1
                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                      ADDRESSEE: INCYTI
STREET: 3174 POR
CITY: PALO ALTO
STATE: CALIFORNI.
COUNTRY: USA
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Pred. No. 1.5e-104;
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Best Local Similarity
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IMMEDIATE SOURCE:
CHORE: SAC0735
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INFORMATION FOR SEQ ID NO: 735:
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LENGTH: 45487 base pairs
TYPE: nucleic acid
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REGISTION NUMBER: 39.132
REFERENCE/DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEPHONE: (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
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ttaattacttgtgatgattacaatgaaaagacaggcg 577
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                                                   GTTAAGCCTACAGATGTAGAAGTTCTGGATGAACAAAAAGGTAAAGATAAACAATTAACA
                                                                gttaagcctacagatgtaggagttctagatgaacaaaaaggtaaagataaacaattaaca
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99.5%;
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Pred. No. 2.3
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RESULT 10
US-60-046-714-734
; Sequence 734, Application US/60046714
; GENERAL INFORMATION:

APPLICANT:

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Best Local :
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ENFORMATION FOR SEQ ID NO: 734:
SEQUENCE CHARACTERISTICS:
LENGTH: 45488 base pairs
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APPLICANT:
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REFERENCE/DOCKET NUMBER: PM-0001-1P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
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IMMEDIATE SOURCE:
CLONE: SAU1c734
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NAME: CERRONE, MICHAEL C.
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CITY: PALO ALTO
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                                                                       gtaagctttgcagaagaaatgaatcactagatgatcaaaatatttcaattgcaggacac
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ACTTTCATTGACCGTCCGAACTATCAATTTACAAATCTTAAAGCAGCCAAAAAAGGTAGT
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Russo, Frank D.
Heath, Joe D.
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US-09-620-608-849
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SEQ ID NO 849
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Best Local Similarity
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APPLICANT: Thornton, Michael
TITLE OF INVENTION: POLYNUCLEOTIDES OF
FILE REFERENCE: PA-0016 US
FILE REFERENCE: PA-0016 US
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OTHER INFORMATION: 813650849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Staphylococcus aureus
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          gtaagtataaaatgacaagtataagagatgttaagcctacagatgtaggagttctagatg
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547;
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3ER: 60/144,883

1999-07-20
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99.3%;
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; OTHER INFORMATION: 8136
; PUBLICATION INFORMATION:
US-60-144-883-849
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US-60-144-883-849
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CURRENT FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 1973
SOFTWARE: PERL Program
SEQ ID NO 849
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chapman, Rowan
APPLICANT: Nuttal, Rachel
APPLICANT: Thornton, Michael
TITLE OF INVENTION: POLYNUCLEOTIDES OF STAPHYLOCOCCUS
FILE REFERENCE: PA-0016 P
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Staphylococcus
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<u>aacaaaaaggtaaagataaacaattaacattaattacttgtgatgattacaatgaaaaga</u>
                  gtaagtataaaatgacaagtataagagatgttaagcctacagatgtagaagttctggatg
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Pred. No. 1.7e-90;
0; Mismatches 3;
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US-09-450-969-1132, Application US/09450969
; Sequence 1132, Application US/09450969
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE; PATH99-09A
; FILE REFERENCE; PATH99-09A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: S.epidermidis
US-09-450-969-1132
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CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO 1132
LENGTH: 612
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Pred. No. 3.
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3.4e-54;
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US-60-068-228-360
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                                                                                                                                                                                                                                                                                                                                                                                                   Matches 455;
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Best Local Similarity
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NFORMATION FOR SEQ ID NO: 360:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: ITBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                 2109
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,1
                                                                                                            2160 TCGACGCCAAAGATACCTTCCGATAAATCTAAAATGGCTGGTTATATAGAAGTTCCAGAC
                                                                                                                                                                                                                                                    2049 ATTTATTTATTCTCAAAGCCATATATCGATAATTATCTACATGAAAAAGATAACGATCAT 2108
                                                                                                                                                                                                                                                                                                                           1989 ATGAAGCAGTGGATGAATAGATTAATCACCTTAATAGGCGTATTGTTAATCATTTTAGCT 2048
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CLONE: SEP1c361
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301 gtaagctttgcagaagaaaatgaatcactagatgatcaaaatatttcaattgcaggacac 360
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CITY: PALO ALTO
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REFERENCE/DOCKET NUMBER: PM-0002-4 P
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VENTION: NUCLEOTIDE SEQUENCES OF STAPHYLOCOCCUS
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Pred. No. 2.2e-52;
0; Mismatches 157;
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CLONE: SE
US-60-038-081-348
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APPLICANT: Corley, Ne
APPLICANT: Russo, Fra
APPLICANT: RUSSO, Fra
TITLE OF INVENTION: I
                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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                                                TOPOLOGY: 1 MOLECULE TYPE:
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              IMMEDIATE SOURCE:
CLONE: SE1c0348
                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                STRANDEDNESS:
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                             NAME:
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Query Match Best Local Similarity

53.4%; 73.2%;

Score 331.4; DB 2 Pred. No. 2.2e-52; 0; Mismatches 157

Indels

Gaps

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DB 28;

Length 11434; 10;

Matches

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Search completed: March 14, 2001, 15:06:48 Job time: 4688 sec

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Lettuce resistance	B. burgdorferi ant		S. pneumoniae PspC			Streptococcus pneu	Plasmodium var-7 p	var-7	Human fetal brain	Plasmodium falcipa	DNA encoding a Sta	DNA encoding a Sta	Human colon cancer	Methanococcus jann		۲,	S. pneumoniae deri	quence encodin	LF(1-254)TRPE(LF(1-254)TRPE(LF(1-254)TRPE(Streptococcus pneu	S. aureus RUSA266	falc			Sequence encoding	P. falciparum tran		Staphylococcus aur	P. falciparum gp19	Borrelia burgdorfe

ALIGNMENTS

V74849;

Staphylococcus 16-MAR-1999

aureus contig SEQ ID #538

(first entry)

V74849 standard; DNA; 3733 BP

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misc_feature Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; 30-JUL-1997 EP786519-A2 misc_feature Staphylococcus toxic shock syndrome; aureus /*tag= b
/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence" /*tag= a
//note= These bases represent a line of missing text in
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are included to maintain the nucleotide numbering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 611; DB 18;
Pred. No: 1.2e-118;
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101 acgataaagattaaagattgaaagattgaacaatatgataaaaatgtaaaagaacaggcga 160

Matches

Similarity

Conservative

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 Query Match
Best Local
                                                            against c
and or
                                                                                                                                  Chicken leucocytozoan immunogenic protein - vaccine against chicken leucocytozoan disease
                                     Sequence 3399 BP; 1577 A;
                                                                                                                Claim 6; Page 6-9; 35pp;
                                                                                                                                                                          WPI; 1996-006311/01.
                                                                                                                                                                                                                          19-APR-1994;
                                                                                                                                                                                                                                            19-APR-1994;
                                                                                                                                                                                                                                                                                 JP07284392-A
                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T05868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T05868 standard;
                                                                                                                                                                                            (DOBU-) DOBUTSUYO SEIBUTSUGAKUTEKI SEIZAI KYOKAI.
(KITA ) KITASATO KENKYUSHO SH.
                                                                                                                                                                                                                                                               31-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                           immunisation; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                               868 encodes a chicken leucocytozoan immunogenic protein, a fragment of it can be used in a recombinant vaccine to inst chicken leucocytozoan disease. The DNA is used in a operatively linked to an expression regulatory sequence
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                                                                                                                                                                R97866.
                                                                                                                                                                                                                                                                                                                                                                                                                    leucocytozoan;
                                                                                                                                                                                                                                                                                                                                                                                                                                     leucocytozoan DNA encoding immunogenic protein
                                                        practice.
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1150..3218
                                                                                                                                                                                                                                                                                              /note= "fragment referred to in the claims, use as insert in a recombinant vacc against chicken leucocytozoan disea
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Score 67.2; DB Pred. No. 1e-05;
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                                                                                                                                                                                                                                                                                                   n a recombinant vaccine leucocytozoan disease"
                                      516 T;
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        Length
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Q87587-89 encode polypeptides having a whole or partial epitope of structural protein of Leucocytozoan protozoa (see R70491-93). The polypeptides and DNA encoding them are useful in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2489
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Q87587
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                                                     Claim 1;
                                                                                                                                                                                                            10-SEP-1993;
                                                                                                                                                                                                                                                              04-APR-1995
                                                                                                                                                                                                                                                                                         JP07089995-A
                                                                                                                                                                                                                                                                                                                Leucocytozoan
                                                                                                                                                                                                                                                                                                                                         leucocytozoan protozoa; struc-
leucocytozoanosis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-1995
                                                                                                                                                                     (DOBU-) DOBUTSUYO SEIBUTSUGAKUTEKI SEIZAI KYOKAI.
(NISS-) NISSEIKEN KK.
                                                                                                                                                                                                                                    10-SEP-1993;
                                                                                       Immune inducing polypeptide against Leucocytozoan protozoa - in production of vaccines for treatment of leucocytozoanosis
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                                                     Page 12-14;
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                protozoa
                                                                                                                                                                                                            93JP-0226078
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        W08601802-A
                                                     exon
                                                             Key
                                                                               Plasmodium
                                                                                                                   Sequence encoding the ring-infected Erythrocyte Surface Antigen (RESA).
                                                                                                                                              24-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                Malaria vaccine; antigen; epitope;
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                                                                                                                                             (first entry)
                       Location/Qualifiers
801.995
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1199.4225
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45.2%;
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                                                                                                                                                                                  ВP
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Pred. No. 1.1e
0; Mismatches
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                                                                                                 SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136
                                                                                                                                                                                                                                                                                                                                                            496
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                                                                                                                                                                                                                                                                                                      667
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RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1984;
11-SEP-1984;
10-SEP-1985;
            X33181;
                                                                                   4186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (N60472) or FRA (N60473). RESA and FIRA antigenicity suitable for providing protective immunity against Plasmodium falciparum malarial infections.
                               X33181 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA coding for E poly:peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1986
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HALL-) HALL INST MED RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-1985;
                                                                                                        498
                                                                                                                                                                                                                                                                                                                                                                    141
                                                                                                                                                                                                                                                                                                                                                                                                  81 acatatcgataattatcttcacgataaagattaaagatgaaaagattgaacaatatgataa 140
                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inventors claim a novel DNA molecule which comprises
                                                                                                                                                                                                                                                                    agtatatccaggaccagcaacacctgaacaattaaatagaggtgtaagctttgcagaaga 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1986-094065/14
                                                                                  aggagttctagatgaacaaaaaggtaaagataaacaattaacattaat
                                                                                                                            tggtaatgaaacacgtaagtataaaatgacaagtataagagatgttaagcctacagatgt 497
                                                                                                                                                                    gaactatcaatttacaaatcttaaagcagccaaaaaaggtagtagtattgtaatttaaagt
                                                                                                                                                                                                               aaatgaatcactagatgatcaaaatatttcaattgcaggacacactttcattgaccgtcc
                                                                                                                                                                                                                                                                                                    agataaatcgaaagtggcaggctatattgaa---attccagatgctgatattaaagaacc
                                                                                                                                                                                                                                                                                                                                                                 aaatgtaaaagaacaggcgagtaaagataaaaagcagcaagctaaacctcaaattccgaa
                                                                                                                                                                                                                                                                                                                                                                                       acatgatgctgaagaaaatgtagaacatgatgctgaagaaaatgtagaagaaaatgttga
                                                                                                                                                                                                                                                          P60569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4590 BP; 1933 A; 437 C; 673 G; 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for Plasmodium falciparum antigens - expressing
le(s) having antigenicity of RESA or FIRA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84AU-0007067.
.84AU-0007066.
85AU-0047326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55pp; English.
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                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%;
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                               6644
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66.4;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ġ,
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saint RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4590;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                        545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cowman
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                                                                                                                                                                                Db
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                                                                                                                                                                                                                                                                                                                                cell line into which an apoptosis resistance gene has been introduced.
The recombinant viruses generated are capable of expressing apoptosis-
associated genes. These can then be used in a variety of diseases for
which the induction of apoptosis by gene transfer, or where the
car inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
are useful as vectors for gene therapy which can be applied to cancer
therapy for destroying cancer cells selectively, the treatment of
cutoimmune diseases and graft rejection reaction, and apoptosis induction
therapy for inflammatory cells in inflammatory diseases. Prior arts have
encountered the problem where if an adenovirus vector capable of
expressing an apoptosis-associated gene is introduced into animal cells,
the cells producing the virus will be destroyed because the period of
time required to induce cell death by apoptosis is shorter than that
crequired to replicate and produce the virus, resulting in fallure to
obtain a recombinant virus having the integrated apoptosis-associated
gene. In this invention an apoptosis-resistant 293 cell line (having an
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 244; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cowpox virus; bsr; viral vector; expression; apoptosis; rescrmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                 3795
                                                                                                                                                                                  3735
                                                                                                                                                                                                                                                                                                                              Sequence 6644
                                                                                                                                                                                                                                                                                                                                                             apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid prayires-bsr, which contains the cowpox virus bsr gene, and is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RPRG-) RPR GENCELL ASIA PACIFIC
                                                                                191
                                                                                                                                               131
                 251
                                                                                                                                                                                                                 71
aagaaccagtatatccaggaccagcaaccactgaaccattaaatagaggtgtaagctttg
                                                                                                                                                                                               ttgctaaaccacatatcgataattatcttcacgataaagataaagatgaaagattgaac 130
                                                 aaattccgaaagataaatcgaaagtggcaggctatattgaaattccagatgctgatatta
                                                                                                               1999-243728/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Page 38-41; 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bsr; viral vector; expression; apoptosis; resistance; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the plasmid pRx-ires-bsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-0259235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-JP04010
                                                                                                                                                                                                                                                                                                                              2166 A; 1573 C; 1424 G;
                                                                                                                                                                                                                                                               9.68;
44.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                               Score 59.8; DB 20
Pred. No. 0.00038;
0; Mismatches 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell
                                                                                                                                                                                                                                                                                                                              1481
                                                                                                                                                                                                                                                 307;
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                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                              0 other;
                                                                                                                                                                                                                                                                              6644;
                                                                                                                                                                                                                                               0;
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                                                 3914
                                                                                250
                                                                                                               3854
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 \begin{array}{c} \texttt{CCCCCCCCCCCXPXXPXXPXPXPXPXDXNNX} \\ \texttt{CCCCCCCCCCXPXPXXPXXPXPXPXNNX} \\ \texttt{CCCCCCCCCXXPXXPXXPXXPXPXPXNNX} \\ \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
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cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4095
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                                                                                                                                                                                                                                                                                                                        07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowpox virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X33182 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4275
                                                                                                                              The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                       Example 2; Page 41-45;
                                                                                                                                                                                                                                                                                                                                                   18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                               WO9913073-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crmA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Base sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999
                                                                                                                                                                                                                                                                    (RPRG-) RPR GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                          HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491
                                                                                                                                                                                   apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bcl-x1; FLIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bsr; viral vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the plasmid pRx-Bcl-xl-bsr
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                                                                                                                                                                                                                                                                                                                          98WO-JP04010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                      51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            survivin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression; apoptosis; resistance;
vin; IAP; ILP; adenovirus; cancer;
                                                                                                                                                                                   cell
                  induction
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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the
                                                                                                                                                                                     5003
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                                                                                                                       X33180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         problem. The present sequence represents the base sequence of plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, is used in an example from the present invention.
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                                                                                                                       standard;
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. No. 0.00039;
ismatches 307;
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0,

crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; autoimmune disease; graft rejection reaction;

Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;

ILP;

inflammation;

Cowpox virus bsr full length gene sequence

25-JUN-1999

(first

entry)

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Best Local Similarity
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5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis associated gene. In this invention an apoptosis resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the cowpox virus bsr gene which
                                                                                                                                                                                                       5008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7797 BP; 2542 A; 1760 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an apoptosis resistant virus sensitive cell line into which an apoptosis resistance gene has been introduced.
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                                                                                                                                                                                                                                                                                                          131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RPRG-) RPR GENCELL ASIA PACIFIC INC
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accgtccgaactatcaatttacaaatcttaaagcagccaaaaaaaggtagtatggtact 430
                                                                                                                                                    aagaaccagtatatccaggaccagcaacacctgaaccaattaaatagaggtgtaagctttg
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Pred. No. 0.00039;
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                         The present invention describes an apoptosis-resistant virus-sensitive (c) cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis. CC associated genes. These can then be used in a variety of diseases for cell inhibition of harmful apoptosis by gene transfer, or where the clinibition of the problem of the problem is therappeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer cell therapy for destroying cancer cells selectively, the treatment of cutorimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of the cells producing the virus will be destroyed because the period of the required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant gene introduced) is established and overcomes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-xl; FLIP; survivin; IAP, ILP; adenovirus; cancer; actoimmune disease; graft rejection reaction; inflammation;
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apoptosis resistant gene introduced) is established and overcomes problem. The present sequence represents the base are sequenced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Base sequence of the plasmid pRx-Bcl 2-i-hCD
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                                                                                  Plasmodium
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                                                                                                                     Sequence encoding
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                                                                                                                                                           Q03875
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                                                                                                                                                                                                                                                                                                   pRx-Bcl 2-i-hCD 25, in an example from
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                                                                                                    falciparum; antigen; malaria; vaccine; GLURP;ss
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1..2352
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                                    /product=GLURP
                                                                                                                     carboxylic terminal part of native GLURP
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                                                                                                                                                                              ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which contains the human Bc1-2
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Best Local Similarity
                                                                                                                                                                                                                                               Matches 239;
                                                                                                                                                                                                                                                                                                                                                                            content of codons for glutamate. Three major repetitive sequences are: one motif from bp 34 to bp 156 is repeated from bp 289 to bp 411; another motif from bp 477 to bp 521 is repeated tandemly twice from bp 1222 to bp 566 and from bp 567 to bp 611; a third motif from bp 1174 to bp 1233 is repeated tandemly 11 times. This last repetitious region consists of 360bp repeats differing only in 3 bases GAT coding for aspartate. This region is flanked to the 5' terminal od a degenerated 60 bp repeat. GC content of the coding part of the insert is on average 30%, and of the non-coding
                                                                                                         1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insert to a "TĀA" stop codon. It is longest ORF found in the sequence. Sequence displays some of the characteristics of other malaria nucleic acid sequences: tandemly repeated motifs, high AT content and a corresponding preference for codons containing these bases, and a high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide(s) derived from Plasmidium falciparum antigen -vaccines and in production of antibodies, for diagnosis and therapy of malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAR-1989;
03-MAR-1989;
                                                                                                                                                                                                                                                                                                                                Sequence 3095 BP; 1443 A; 300 C; 491 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An open reading frame of 2349 bps extends from the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 7; 108pp; English
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                                                                                                                       atatgataaaaatgtaaaagaacaggcgagtaaagataaaagcagcaagctaaacctca 191
agaaccagtatatccaggaccagcaacacctgaacaattaaatagaggtgtaagctttgc
                                                     aattccgaaagtagaaagtggcaggctatattgaaattccagatgctgatattaa
                                 aatagtagaggttgaagaaattctaccagaagataaaaatgaaaaagttgaacatgaaat
                                                                                                    tgaaatagtagaagttgaagaaattctaccagaagataaaaatgaaaaaggtcaacatga
                                                                                                                                                                         tgaaatagtagaggttgaagaaattctaccagaagatgataaaaatgaaaaaggtcaaca
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                                                                                                                                                                                                                                               Conservative
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89DK-0005191
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 Mismatches

                                                                                                                                                                                                                                            Score 56.6; DB 11;
Pred. No. 0.0016;
0; Mismatches 304;
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                                                                                                                                                                                                                                                                                                                                 861 T; 0 other;
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                                                           Matches
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Best Local :
                                                                                                                                                                         This sequence corresponds to the coding sequence for a Plasmodium falciparum strain KI pre-erythrocytic liver stage antigen-3 (LSA-3) protein. The gene sequence was isolated by screening a P. falciparum strain T9/96 library with serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 7295 was used to screen a library generated from Thai strain KI. One clone contained a 6.85 kb insert including the genomic sequence T78867. The gene comprises a 1.8 kb region encoding 3 major blocks of 4 amino acid repeats and a 3' hydrophobic region corresponding to a 91ycosyl-phosphatidylinositol membrane anchoring sequence. The invention relates to new polypeptides of at least 10 amino acids derived from the LSA-3 polypeptide with the exception of the peptides W24791-4. The LSA-3 peptides can be used to raise antibodies and as vaccines for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum; pre-erythrocyte; liver stage antigen; serum; prophylaxis; Thai strain; gene organisation; exon; intron; hydrophob; glycosyl-phosphatidylinositol membrane anchoring sequence; antibody;
Plasmodium falciparum poly:peptide(s) and related nucleic acids derived from the liver stage antigen-3, useful for malaria vacci prodn. and diagnosis
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                | 104 ataaagattaaagattgaacaattgataaaaatgtaaaagaacaggcgagta 163
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47.2%;
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Pred. No. 0.00
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hydrophobic;
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glycosyl-phosphatidylinositol membrane anchoring se
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13-JUN-1995;

95FR-0007007

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (W24790). The gene sequence was isolated by screening a P. falciparum strain T9/96 library with the serum from a missionary treated by prophylaxis (for strain T6/96 see FR9101286). Of 20 clones isolated, clone 7295 was used to screen a library generated from Thai strain K1. One clone contained a 6.85 kb insert including the sequence presented here. The gene organisation comprises a first exon, a short 168 bp intron and a 5 kb second exon containing a 1.8 kb region encoding 7 blocks of 4 amino acid repeats and a 3' hydrophobic region corresponding to a glycosyl-phosphatidylinosicol membrane anchoring sequence. The invention relates to new polypeptides of at least 10 amino acids derived from the LSA-3 polypeptide with the exception of peptides W24791-4. The LSA-3 peptides can be used to raise antibodies
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   5193
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i. No. 0.0018;
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T41852

T41852 standard; DNA; 9

AC T41852;

XX 20-FEB-1997 (first ent
XX 20-FEB-1997 (first ent
XX Plasmodium falciparum;
XW plasmodium falciparum;
XW plasmodium falciparum;
XW detection; identificati
XX Plasmodium falciparum M
XX Key Locatio
FT CDS 126..94
FT CDS 326..94
FT CDS 126..94
FT misc_feature 518..52
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FT misc_feature 7/409..
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  New Plasmodium falciparum erythrocyte membrane proteins -
                                                                                                                                           (AFFY-) AFFYMAX TECHNOLOGIES
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identification; treatment; prevention; pa
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6257..6259
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6254..6256
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DT 04-MAY
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Best Local :
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malaria
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 epidemic relapsing fever; endemic relapsing fever; infection; diagnosis; characterisation; detection;
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                            Borrelia burgdorferi; spirochete; bacterium;
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parasite
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                                                                                     (first entry)
                                                                                                                                           DNA;
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                           pathogen; Lyme disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 910715 BP; 327171 A; 129646 C; 130753 G;
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22-JUL-1997;
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97US-0053344.
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                                                                                                                                           surface protein). This gene is used in a method for stabilising the gene sequences by reducing the AT content. Such products are useful in vaccines against malaria or for producing monoclonal antibodies (for passive immunisation). The complete gp190 protein can now be produced outside the parasite and has, at least over extended regions, the native pattern of folding. Larger amounts of the protein can be produced recombinantly than would be possible using the parasites as source.
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be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides of the control of the co
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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ALIGNMENTS

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                                                                                                              TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
COMPUTER: HP Vectra
OPERATING SYSTEM: MS
                                                                                                                                             TELEPHONE: (301) 309-8504
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                             SEQUENCE CHARACTERISTICS:
                                                             LENGTH:
TYPE: a
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CITY: Rockville
STATE: Maryland
                                                                                                                                                                             NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                              STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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QVSDDPDAVYGYLSIPSLEIMEPVYLG-ADYHHLGMGLAHVDGTPLPLDGTGIRSVIAGH 110

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Query Match Best Local Similarity

12.7%;
30.8%;

Matches

45;

Conservative

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Score 137; DB Pred. No. 8.8e-23; Mismatches

DB 3; 8e-07;

Length 223; Indels

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                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
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 335 LKNGKVFDKNTSGKPFAFKLGRGEVIKGWDIGVAGMSVGGERRIII 380
                                                                                                                                              226 DNDGEEEQEEEEEEQKEEVKPEPKKSKKEKKRKHEEKEEEKKAK--KVKKVEFKKDLEE 283
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                                                                       284 GPTKPKSKKEQDKHKPKSKVLEG-GIVIEDRTIGDGPQ-----AKRGARVGMRYIGK 334
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                                                                                                         90 GPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFK-VG- 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Woodcock Washburn Kurtz Mackiewicz & One Liberty Place - 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandes-Alnemri, Teresa
VENTION: IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING
                                                                                                                                                                                                                                                                                                                                                                                                                                           215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Litwack,
                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                   linear
                                     -NETRK----YKMTSIRDVKPTDVGVLDEQKGKDKQLTL 181
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21.1%;
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Emad S.
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37; Mis
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                                                                 Sequence 2, Application Patent No. 5854416
GENERAL INFORMATION:
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Best Local Similarity 28.0%;
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INFORMATION FOR SEQ ID NO:
                    APPLICANT:
                                   APPLICANT:
                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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     APPLICANT:
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SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                             AFKYFSKAYG----VPSAYIWEINTEEEGTPEQIKTLVEKLRQTKVPSLFVE--SSVDDRP
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                                                                                                 Application US/08715131
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Sampson, Jacquelyn S.
Russell, Harold
Tharpe, Jean A.
Ades, Edwin W.
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APPLICANT:

Carlone, George M.

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; MOLECULE TYPE:
US-08-715-131-2
                                                                                                                                                                                                                                                                                                                                US-08-922-837-2
                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08922837 Patent No. 5888770
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Best Local
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                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                      APPLICANT: Chalker,,
APPLICANT: Feliu,, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                      APPLICANT: Bryant,, Alexander P. TITLE OF INVENTION: NO. 5888770el SpoIIIE NUMBER OF SEQUENCES: 2
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                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                                                                                  262 MKTVSQDTNIPIYAQIFTD-----SIAEQGKEGDSYY-----SMMKYNLDKIAE 305
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                                                                                           STREET: 4000 CITY: Philadelphia
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                   COUNTRY: USA
ZIP: 19103-2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                       ADDRESSEE:
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Brown,, James R.
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127 Peachtree Street, Suite 1200
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IBM Compatible
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UMBER: 36,016
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28.0%; Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09196857A Patent No. 6100069
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Best Local Similarity
                                                                                                    APPLICANT: Zhong, YiYi
APPLICANT: Debouck, Christine
APPLICANT: Jaworski, Deborah D.
                 APPLICANT: Warren, Richard L.
APPLICANT: Schilling, Lisa K.
TITLE OF INVENTION: NO. 6100069e1
FILE REFERENCE: GM10118
CURRENT APPLICATION NUMBER: US/09/196,857A
                                                                                                                                           APPLICANT: Mooney, Jeffrey APPLICANT: Zhong, YiYi
                                                                                                                                                                               APPLICANT: Lawlor, Elizabeth J.
                                                                                                                                                                                                APPLICANT: Throup, John P.
                                                                                                                                                                                                                                        APPLICANT: Brown, James
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                                                                                       APPLICANT: Wang, Min
                                                                                                                                                                                                                   APPLICANT: Biswas, Sanjoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 LIGVALYIPTAFLFS--NIGTYFIGSILILVGSLLVSPWSVYDIAEFFSRGFAKWWEGHE 213
                                                                                                                                                                                                                                                                                                                                                                                                        344 LEAT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                            200 FVAT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRKI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 RRKEERFVKQEEKARQKAEKEAR-----LEQEETEKA-LLDLPPVDMETGEILTEEAVQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 NLPPIPEEKWVEPEIILPQAELKFPEQEDDSDDEDVQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dickinson, Q. Todd REGISTRATION NUMBER: 28, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 PGPATPEQL------NRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 KDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADI-----KEPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 IAGVVLILVAAYLFAKPHIDNYL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                         Zalacain, Magdalena
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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17.2%;
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Pred. No. 2
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EARLIER APPLICATION NUMBER: 60/082,418

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08285440 Patent No. 5532337
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Best Local
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                                                                                                                                                           APPLICATION NUMBER: 07/858,94
FILING DATE: MATCh 27, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                         INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DC SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
MOLECULE TYPE: peptide
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 ETVDVIVTFPE--DYQAEDL-AGKEAKFV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 AKDIDEEVETLADLKEK 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 TVVID---FVGSIDGVEFD------GGKGENFSLGLGSGQFIPGFEDQ---LVGHSAG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 VIAAEVVTKPEVKLGDYKNLEVSVDVEKEVTDADVEERIERERNNLTELVIKEAAAENGD 164
                                 STRANDEDNESS:
                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 QIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGH--- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 LVAAYLFAKPH-------IDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKP 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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                                                                      LENGTH:
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                                                       amino acid
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                                                                    558 amino acids
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805 Fifteenth Street, N.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQK 173
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                      linear
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                                   single
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                                                                                                                                                                                                                                                                                    07/858,947
                                                                                                           6.
                                                                                                                                                                                                                                                                                                                                                                                                                                               5.25 inch, 500 kb
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; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-6
                                                                                                                                                                                                                                                                       US-08-630-349-6
                                                                                                                                                                                                                                                                                                                                                                                             Db .
                                                                                                                                                                                                                                           Sequence 6, Application US/08630349 Patent No. 5739008
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Best Local
                                                                                                                                                                                                                             GENERAL INFORMATION:
                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
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                                                                                                                                                                                               APPLICANT: Ken'ichiro HAYASHI et al. TITLE OF INVENTION: POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
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                                                                                                                                                                                   NUMBER OF SEQUENCES:
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IMMEDIATE SOURCE:
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                                                                                 CITY: ...
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                 228 IKDEKIKKDKEPKEEVKSFMDRKKGFTEVKSQNGEFMTHKLKHTENTF-SRP
                 COMPUTER:
OPERATING
                                                                                                                   CITY: Washington
                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                           78 IPDADIKEPVYPGPATPEQLNRGVSFAE---ENESLDDQNISIAGHTFIDRP 126
                                                                                                                                                                                                                                                                                                                                                                                                                        30 DNYLHDKDKDEKIEQ-----YDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIE 77
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CELL TYPE:
   SOFTWARE:
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                                                                            20005
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                                                                                                                                  E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W.,
                 IBM Compatible SYSTEM: MS-DOS
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Wordperfect 5.1
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25.9%;
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Pred. No.
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CURRENT APPLICATION DATA:

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                                                                                TELEFAX: (415)343-434
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCBS
TELECOMMUNICATION INFORMATION:
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NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                               SEQUENCE CHARACTERISTICS: LENGTH: 759 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 IKDEKIKKDKEPKEEVKSFMDRKKGFTEVKSQNGEFMTHKLKHTENTF-SRP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07 FILING DATE: March 27,
                                                                                                                                                                                                               CLASSIFICATION: 530
                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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                  STRANDEDNESS:
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Best Local Similarity
Matches 35; Conserv
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Best Local
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LENGTH: 759 amino acids
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NUMBER OF SEQUENCES:
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                                                              227 DMEEEENDDDDDDDDEEDGVFDDEDEEEENI----ESKVTKPVQIQKRAVKR----PAPAKS 280
281 SDHSEEDSDLEESDSIDDGEELAQSDTSTEEQEDKAVQVSNKKKR-----KLPSDVNEGK 335
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                             EQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYK 154
                                                                                               DKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATP
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Pred. No. 4.5;
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                                                                 GENERAL INFORMATION:
                                                                                     Sequence 20, Appli
Patent No. 6022739
                APPLICANT: Ryan, Clarence A APPLICANT: Pearce, Gregory L APPLICANT: McGurl, Barry F
TITLE
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INFORMATION FOR SEQ ID NO:
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LENGTH: 759 amino acids
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TELECOMMUNICATION INFORMATION:
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NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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LENGTH: 190
TYPE: PRT
ORGANISM: Capsicum annuum
US-08-881-094-20
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Best Local Similarity
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EARLIER FILING DATE: 1991-05-24
NUMBER OF SEQ ID NOS: 43
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EARLIER FILING DATE: 1993-03-18
EARLIER APPLICATION NUMBER: 07/885,412
EARLIER FILING DATE: 1992-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/881,094A CURRENT FILING DATE: 1997-07-09 EARLIER APPLICATION NUMBER: 08/308,887 EARLIER FILING DATE: 1994-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
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EARLIER FILING DATE: 1990-05-25
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APPLICANT:
APPLICANT:
              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                         FILING DATE: Filed HOPRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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ADDRESSEE: Incyte Ph
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TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
NUMBER OF SEQUENCES: 7
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                                                                            FILING DATE:
                                                                                                                                 APPLICATION NUMBER: US/08/7 FILING DATE: Filed Herewith
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OPERATING SYSTEM:
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  REFERENCE/DOCKET NUMBER:
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5874286
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3174 Porter Drive
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Goli, Surya K.
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PF-0126 US
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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               TELECOMMUNICATION INFORMATION:
                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer.
APPLICANT: Zweiger, Gary B.
TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
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1072344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 QFTNLKAAKKGSMVYFK------VGNETR-----KYKMTSIRDVKPTDVGV 168
                        NAME: Billings, Lucy J.
REGISTRATION.NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0126
                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                                                                                APPLICATION NUMBER: US/09/162,597 FILING DATE:
                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                       MEDIUM TYPE:
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415-855-0555
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Pred. No.
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US-08-137-175A-5
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Best Local Similarity
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                                                        FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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                                         TELECOMMUNICATION INFORMATION:
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TELEPHONE: 202 -- 3528
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STRANDEDNESS: si
                                                                                                                        APPLICATION NUMBER: PCT/US92/08972 FILING DATE: 22-OCT-1992
                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                     APPLICATION NUMBER:
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5777095
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                                                                                                                                                                                                                                                                                                                 20004
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419 Seventh Street, N.W.,
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                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BERGSTROEM, Sven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARBOUR, Alan G.
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26-OCT-1993
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IMPROVEMENT IN
                                                                                                                                                                                                                                 Release #1.0,
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Pred. No. 1
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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-137-175A-5
Search completed: March 2, 2001, 10:23:05 Job time: 87~{\rm sec}
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                                                             53 SLKATVDKIELKGTSDKDNGSGVLEGTKDDKSKAKLTIADDLSKTT--FELFKEDGKTLV 110
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ALIGNMENTS

RESULT Y00252

Y00252;

Y00252 standard; Protein; 251 AA

Enterococcus faecalis protein EF130.

20-APR-1999 (first entry)

14-NOV-1997; 06-MAY-1997; 16-MAY-1997; New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection WPI; 1999-070095/06 N-PSDB; X20242. 04-MAY-1998; Enterococcus faecalis Bailey C, Choi GH, (HUMA-) HUMAN GENOME SCI INC 12-NOV-1998. WO9850554-A2 detection; attenuation; antigenic. Enterococcus faecalis; infection; vaccine; immune response; diagnosis; 97US-0066009. 97US-0044031. 97US-0046655. 98WO-US08959 Hromockyj A, Kunsch CA;

37 kDa

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Best Local
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06-MAY-1997;
16-MAY-1997;
        New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening
                                                                N-PSDB;
                                                                                                     Bailey
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52; Conservative
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                                                 N-PSDB;
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detection; attenuation;
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06-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lqekmekknqelakkgsnpgldpfsetqkttkkpdksyfeshtigvltipkinvrlpif- 119
                                                                                     Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
56; Conserv
                                                 X20243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s can be used for detecting Enterococcus nucleic acids. from the present invention can also be used for screening to identify agonists and antagonists of E. faecalis prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 169; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                               faecalis antigenic polypeptide fragment EF130
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                    97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                        98WO-US08959
                                                                                     GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.7%;
25.3%;
                                                                                     Hromockyj
                                                                                                                                                                                                                                                                                                       infection; vaccine;
                                                                                                                                                                                                                                                                                           antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 158.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                     Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                       immune response; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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7;

New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection

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Best Local
                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis;
detection; attenuation;
                                                                                                                                                                                                                                                                           Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of {\rm E.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                  Claim 9; Page 170;
                                                                                                                         New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in
                                                                                                                                                                                                      N-PSDB; X20149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9850554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus
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                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN
                                                                                               for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 itcgdlgattriavggtlaattpik 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 FIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTL | : |: |: |: :| |: :| |: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
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les 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4-
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                                                                                                                                                                                                                           1999-070095/06
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                                                                                                                                                                                                                                                                           Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               faecalis antigenic polypeptide fragment EF079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        faecalis
                                                                                                                                                                                                                                                                                                                                GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                             97US-0066009.
97US-0044031.
97US-0046655.
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                                             301pp;
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27.68;
                                                                                                                                                                                                                                                                           Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection;
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                                               English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
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Pred. No. 1.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
                                                                                                                                                                                                                                                                              Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response; diagnosis;
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                                                                                                 infection
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The present sequence represents an antigenic polypeptide fragment

The present sequence represents a protein from Streptococcus pne The nucleic acid sequence encoding the Streptococcus pneumoniae

pneumoniae iae protein

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W61218
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Best Local
                                                                                                                   WPI; 199
N-PSDB;
                                                                                                                                                           Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample
                                                              Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W61218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for
                                     Claim 11; Page 82; 118pp; English
                                                                                                                                                                                                              31-OCT-1996;
                                                                                                                                                                                                                                                                  07-MAY-1998
                                                                                                                                                                                                                                                                                           WO9818930-A2
                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W61218 standard;
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                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                       30-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 l-ftdlpelkkgdefyievngktlayqvdqiktveptdtkdlhiesgqd-lvtlltctpy
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                                                                                                                   1998-272224/24.
DB; V27404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENE---SLDDQNISIAGHTFIDRPN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          htigvltipkinvrlpif-dktnalllekgssllegtsyptggtnthavisghrglpqak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 25.4
46; Conservative
                                                                                                                                                          Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                                               pneumonia; otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae; antigen; vaccine; infection; diagnosis;
pumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae SP0093 protein.
                                                                                                                                                                                                              96US-0029960
                                                                                                                                                                                                                                       97WO-US19422
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    /note= "encoded by GNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                   /label= unknown
                                                                                                                                                          A
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                                                                                                                                                           Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 146; DB 20;
Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                          ĽS,
                                                                                                                                                          Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT
W89768
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Best Local
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                                           WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer readable medium; vaccine; S.aureus infection; immuno cellulitis; eyelid infection; food poisoning; osteomyelitis; skin infection; surgical wound infection; scalded skin syndrous infection; scalded skin syndrous
                                                                                              Barash SC,
Rosen CA;
                                                                                                                                                                                                                                                                                 07-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                     EP786519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus protein SEQ ID #5216
                                                                                                                                                                                                                              05-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W89768
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                                                                                                                                                                          (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                     30-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt r\text{-}aepshvffrhldqlkvgdalyydngqeiveyqmmdteiilpseweklesvsskn\text{-}imt}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qvsddpdavygylsipsleimepvylg-adyhhlgmglahvdgtplpldgtgirsviagh 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENE-SLDDQNIS--IAGH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
45; Conserv
                                                                                                                       Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                          GENOME
                                                                                                                                                                                                                              96US-0009861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus
                                                                                                                                                                                                                                                                                 97EP-0100117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%;
                                                                                                                                                                          SCI
                                                                                                                       Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "these residues represent a line of missing te
in the sequence listing in the specification.
They are included to maintain the residue
numbering given in the specification for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EKTGVWEK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 137; DB 19;
Pred. No. 1.1e-05;
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                                                                                                                    Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                    Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             text
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identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, foo poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The DNA sequences (and their fragments) are useful as primers or
                                                                                                                                                                                                                                                                                                                 disk, random access memory (RAM), read-only memory (ROM) or cD-ROM. Homology searches using the Saureus Die Gequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been industriated and the sequences of the sequences which are likely to encode antigens have been industrial and the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             on a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
Sequence
                                                  contained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 3213-3214; 3271pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          ntion. The DNA sequences encoding the S.aureus protein sequence computer readable medium, preferably selected from a floppy, random access memory (RAM), read-only memory (ROM) togy searches memory (RAM).
                                                                           for isolating homologues of any of the 5191 S. aureus DNA sequences
                                                     on
167
ΑĄ
                                                     computer readable medium
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of the ins are recorded a floppy or hard
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Query Match
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Matches 40
Y20763;
                       Y20763
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                                                                                                            180 TLITCDDYNEKT
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                                               . 7
                                                                                                                                                                                                                                 sqdksddnqkkt
                                                                                                                                                            HTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQL 179
                                                                                                                                                                                     qeekeqneldsqanqyqqlpqqnqyqyvppqqqaptk--
                                                                                                                                                                                                              QAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAG 119
                      standard;
                                                                                                                                                                                                                                                                                            40;
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                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                            Conservative
                       Protein;
                                                                                       160
                                                                                                               191
                                                                                                                                                                                                                                                                                                     8.4%; Score 90; DB 18; 20.8%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                 Length 167
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                                                                                                                                                                                                                                                                                         64;
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RESULT
Y20763
glial f
bcl-2;
                                                                                                           frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Taubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M; neurofilament-F; presenilin II; cellular tumour antigen;
                              Synthetic
                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                           Húman neurofilament-M mutant protein fragment 45.
                                                                                                                                                                                                                                                                                             22-JUL-1999 (first entry)
                                                                            fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
                                                                                                                                                                                                                        beta-amyloid precursor protein; beta-APP; diagnosis;
                                                               group protein-C;
                                                               neuroendocrine
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cancer;

sapiens

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RESULT
W68011
ID W6
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AC W6
XX
DT 27
DT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC This invention describes a novel method for the diagnosis of a disease CC caused by, or associated with, an RNA molecule that has a frameshift CC mutation. The method is used to diagnose age-related diseases, especially CC cancer and a wide range of neurodegenerative disorders (e.g. Alzhelmer's CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease, CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II CC and many others listed) or susceptibility to these disorders. The method CC allows a definitive diagnosis of Alzhelmer's disease in living pattents, CC at an early stage. It is based on the observation that disease may be CC caused by mutations in RNA rather than DNA. The invention describes the CC used of neuronal system RNA molecules, specifically proteins including CC beta-amyloid procursor protein (beta-APP), the microtubule associated CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule CC associated protein 2 (MAP2), neurofilament-L, neurofilament-R, CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma CC protein-C (HMGP-C) and neuroendocribe specific protein abolility group CC protein-C (MGPC) and neuroendocribe specific protein a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; X75759
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(ROYA-)
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      Yeast
                                                               27-APR-1999
                                                                                                                              W68011
                                                                                                                                                                                    W68011 standard; Protein; 411 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIP-----
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   immunophilin FKBP46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
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ROYAL NETHERLANDS ACAD
UNIV ROTTERDAM ERASMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grosveld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0043163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-IB00705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroendocrine specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 90; DB
Pred. No. 1.4;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Leeuwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394
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PD XXX XXX ACC

W09927105-A2

В Qγ Вр Qy В οy

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RESULT
Y35617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated immunophilin FKBP46 nucleic acids - useful for developing products for the study and identification of immunosuppressive agents for treating e.g. transplant and tissue graft patients
                               sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Column 25-38; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995;
31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunophilin; moth;
transplant; tissue (
Chlamydia pneumoniae
                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                              Chlamydia pneumoniae surface exposed polypeptide
                                                                                                                                                      13-SEP-1999
                                                                                                                                                                                                                               Y35617 standard; Protein; 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agents can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that bind to it. Such immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the immunophilin FKBP46 from the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; X04444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-130433/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                  148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
                                                                                                                                                                                                                                                                                                                          335 lkngkvfdkntsgkpfafklgrgevikgwdigvagmsvggerriii 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYP
                                                                                                                                                                                                                                                                                                                                                              -----NETRK---YKMTSIRDVKPTDVGVLDEQKGKDKQLTL
                                                                                                                                                                                                                                                                                                                                                                                                  gptkpkskkeqdkhkpkskvleg-giviedrtigdgpq----akrgarvgmryigk
                                                                                                                                                                                                                                                                                                                                                                                                                                       GPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFK-VG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411
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                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JEFFERSON THOMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0007163.
96US-0741134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0741134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in treating transplant and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insect cell; nuclear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 89.5;
Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Litwack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppression; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive
tissue graft patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                              , 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                 W98324
                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
           29-JUL-1997;
01-APR-1997;
24-JUN-1997;
                                                                                                                                                         GHPO protein;
peptic ulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease, sarcoidosis, sinusitis, purulent offitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see Y34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see X91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart
                                                            01-APR-1998;
                                                                                                                                                                                                                       31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1998;
21-NOV-1997;
                                                                                    08-OCT-1998
                                                                                                                                  Helicobacter
                                                                                                                                                                                                                                             W98324;
                                                                                                                                                                                                                                                                    W98324 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 1344-1347; Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-357842/30
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                                                                                                                                                                                                                                                                                                                                                       152
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                                                                                                                                                                                                                                                                                                                                265
                                                                                                                                                                                                                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                            pylori
                                                                                                                                                                                                                                                                                                                                                      KYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDYNE 189
                                                                                                                                                                                                                                                                                                                                                                                                                          vsekissdtkenrkdletedpskksglkevssdlpkspetavaaisedleisenisardp
                                                                                                                                                                                                                                                                                                                              ----sdrdivfenl-----vkglsfiscesled 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLN------
                                                                                                                                                                                                                                                                                                                                                                         lqqlaffykntssqsisekdssfqgiifsgsgansglgfenlkapksgaavy------
                                                                                                                                                                                                                                                                                                                                                                                            -RGVSFAEEN---ESLDDQNISIAGHTFID---RPNYQFTNLKAAKKGSMYYFKVGNETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
39; Conserv
                                                                                                                                                                                               GHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                    (first entry)
                                                                                                                                  pylori
                                                                                                                                                        disease.
                                                                                                                                                                    Helicobacter infection; gastroduodenal disease;
            97US-0902615.
97US-0833457.
97US-0881227.
                                                                                                                                                                                              1411
                                                           98WO-US06371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-IB01890.
                                                                                                                                                                                                                                                                    Protein; 359
                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%;
24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89.5; DI
Pred. No. 7.2;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1912pp;
                                                                                                                                                                                                                                                                    AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                      gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           212
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RESULT
W55072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
          Choi GH,
                                                                                   30-OCT-1997;
                                                                                                                                                                                 Streptococcus pneumoniae; antigen; vaccine; detection; pneumonia; otitis media; meningi
                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                                                                               02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Helicobacter polynucleotides - for the diagnosis, prevention and treatment infections and gastrointestinal diseases
                                  (HUMA-) HUMAN GENOME SCI INC
                                                           31-OCT-1996;
                                                                                                           07-MAY-1998
                                                                                                                                    WO9818930-A2
                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                        W55072
                                                                                                                                                                                                                                                                                              W55072 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 435-437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC. (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                  152 KYKMTSIRDVK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                  117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 FAKPHIDNYLHD--KDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIP--
                                                                                                                                                                                                                                                                                                                                                         ky----indkk 357
                                                                                                                                                                                                                                                                                                                                                                                                        vlsrigkahlghvfndgpkelgglrycinsaalrfiplkdmekegygefipyikkg-elk 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                       neyynkee egiyv \texttt{dittgeplfssadkydsgcgwpsfskpinkdvvkyeddeslnrkrie}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998-542293/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
          Hromockyj A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AGHTFIDRPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kleanthous H,
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                      pneumoniae SP0013 protein
                                                                                                                                                           pneumoniae
                                                           96US-0029960.
                                                                                   97WO-US19422
                                                                                                                                                                                                                                                                                               Protein; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DADIKEPVYPG------PATPEQLNRGVSFAEENESLDDQNIS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2054pp; English.
          Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miller C,
                                                                                                                                                                                  media; meningitis.
                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               -YOFTNLKAAKK---GSMV-YFKVGNETR 151
          Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to develop
of Helicobacter
                                                                                                                                                                                             infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
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                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 19
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 52; 118pp; English
                                                                                                                                                                                     WO9945121-A1
                                                                                                                                                                                                                Streptococcus
                                                                                                                                                                                                                                              Pneumoccocal surface adhesion A protein; PsaA; monoclonal antibody; vaccine; Streptococcus pneumoniae infection.
                                                                                                                                                                                                                                                                                        37 kDa pneumoccocal
                                                                                                                                                                                                                                                                                                                     09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                  Y30350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         can be useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protective or therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in
                                                                                                   02-MAR-1998;
                                                                                                                              26-FEB-1999;
                                                                                                                                                           10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                              Y30350 standard; Protein;
                            Zeiler
                                          Ades EW,
                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (especially 10-300) mu g/ml per dose
                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 LFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASK----DKKQQAK-PQIPKDK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid sequence encoding the Streptococcus pneumoniae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mktvsqdtnipiyaqiftd-----siaeqgkegdsyy-----smmkynldkiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          afkyfskayg--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-272224/24.
DB; V27333.
1999-540849/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ifak-niakqlsakdpnnk-efyeknlkeytdkldkldkeskdkfnkipaekklivtseg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD 160
                                          Carlone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a protein from Streptococcus
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                 pneumoniae
                                                                                                  98US-0076565
                                                                                                                              99WO-US04326
                                          GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·vpsayiweinteeegtpegiktlveklrqtkvpslfve--ssvddrp
                                                                                                                                                                                                                                                                                        surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2%;
28.0%;
                                                                                                                                                                                                                                             pneumoniae
                                          Sampson
                                                                                                                                                                                                                                                                                                                                                                              309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for inducing protective antibodies against for treatment or prevention of infection e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                       adhesion A protein (PsaA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                             A
                                          JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                       Tharpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for diagnosis
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                        JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                        Westerink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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DR PT PT SXX
RESULT 13
W82496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                      17-SEP-1996;
17-SEP-1991;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a pneumoccocal surface adhesion A pro (PsaA). The specification describes monoclonal antibodies which bind epitopes of the PsaA protein (see Y30351-54). These peptides can be used in vaccines to prevent Streptococcus pneumoniae infections. The antibodies of the invention can also be used to detect S. pneumoniae a sample or individual.
                                             Nucleic acid encoding the 37 pneumoniae - useful diagnost
                                                                                                                                                                                                                                                                                                                         S. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                      W82496;
                                                                                                                                                                                                                                                                                                                                                                                           W82496 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Z10411.
                                            pneumoniae
                                                                            N-PSDB;
                                                                                                             Ades EW,
                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                   17-SEP-1996;
                                                                                                                                                                                                                         29-DEC-1998
                                                                                                                                                                                                                                               US5854416-A
                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                          diagnostic;
                                                                                                                                                                                                                                                                                                    Surface adhesion A protein;
                                                                                                                                                                                                                                                                                                                                                04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subject
                                recombinant polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 mktvsqdtnipiyaqiftd-----siaeqgkegdsyy----smmkynldkiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 -----SKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS------FAEENESLDDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASK----DKKQQAK-PQIPKDK------
                                                                           1999-095007/08.
DB; V73914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             afkyfskayg---vpsayiweinteeegtpeqiktlveklrqtkvpslfve--ssvddrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conserv
                                                                                                             Carlone GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 53-54; 58pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                        immunoassay;
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NISIAGHTFIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRD
                                         encoding the 37 kDa. surface adhesion A of useful diagnostically and for production c
                                                                                                                                                                                                                                                                                                                        37-kDa surface adhesion A protein
                                                                                                                                                     96US-0715131.
91US-0791377.
94US-0222179.
                                                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                                                                   96US-0715131
                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.2%;
                                                                                                             Russell
                                                                                                                                                                                                                                                                                           treatment;
                                                                                                                                                                                                                                                                                                                                                                                            309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to Streptococcus pneumoniae PsaA, u Streptococcus pneumoniae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 88.5; DB Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                             Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                          Sampson
                                                                                                                                                                                                                                                                                        detection; serotype; antibody;
infection; anti-idiotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB
                                                                                                             JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
                                                                                                           Tharpe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                          f Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used
                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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Claim 1; Column 33-34; 20pp;

English

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RESULT 14
Y81668
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a Streptococcus pneumoniae 37-kDa surface adhesion A protein. This encoding nucleic acid can be used in methods to express recombinant protein, as a source of primers for amplification (to identify and isolate related sequences, e.g. alleleic variants) or probes for nucleic acid hybridisation tests for detecting S. pneumoniae, and in DNA vaccines. This protein and its fragments can be used to raise antibodies, in vaccines and for detecting S. pneumoniae (by reaction with specific antibodies). Antibodies are useful in diagnostic immunoassays, to treat infections and to raise anti-idiotype antibodies for use in vaccines. This protein is very highly conserved between the different serotypes of S. pneumoniae so is an excellent candidate for vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumon antibacterial; antiin pneumococcal disease.
specifically
                                                                                                                                New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents or inhibiting expression of the protein -
                                                                                                                                                                                                                          WPI; 2000-195300/17.
                                                                                                                                                                                                                                                                    Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                           27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development.
                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y81668 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                       isolated
                                                                                                                                                                                                                                                                                                               (MICR-) MICROBIAL TECHNICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASK----DKKQQAK-PQIPKDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ifak-niakqlsakdpnnk-efyeknlkeytdkldkldkeskdkfnkipaekklivtseg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             afkyfskayg---vpsayiweinteeegtpeqiktlveklrqtkvpslfve--ssvddrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQ-
                                                                                       6; Page 90; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
to Y81679 represent specifically claimed protein sequences ed from Streptococcus pneumoniae. A05407 to A05590 represenically claimed nucleotide sequences isolated from S. pneumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD
                                                                                                                                                                                                                                                                    Hansbro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae protein sequence ID205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                           98GB-0016337
99US-0125164
                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-GB02451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.2%;
28.0%;
                                                                                                                                                                                                                                                                      PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---siaeqgkegdsyy----smmkynldkiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 88.5; DB Pred. No. 0.88;
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                                                                                                                                                       capable
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                                                                                                                                                   for diagnosis of capable of antagon
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  pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. A05591 to A05614 represent primers used in the exemplification of the present invention.
The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describgenes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuation.
                                                                                                New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                           14-NOV-1997;
06-MAY-1997;
                                                                      Claim
                                                                                                                                                           N-PSDB;
                                                                                                                                                                        WPI; 1999-070095/06
                                                                                                                                                                                                   Bailey C,
                                                                                                                                                                                                                                (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                      04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus
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                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                        attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               faecalis antigenic polypeptide fragment EF106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                 GENOME SCI INC
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                   GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 310
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                                                                                                                                                                                                   Hromockyj.A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                      antigenic
                                                                     English
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response;
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CC infection caused by a member of the Enterococcus genus in an animal.

CC They can also be used for detecting Enterococcus antibodies in a sample.

CC The nucleotide sequences can be used for detecting Enterococcus nucleic cc acids. Products from the present invention can also be used for CC screening compounds to identify agonists and antagonists of E. faecalis cc protein activity.

XX SQ Sequence 310 AA;

Query Match 8.1%; Score 87; DB 20; Length 310; Best Local Similarity 25.7%; Pred. No. 1.2; Matches 28; Conservative 20; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 20; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 20; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Conservative 30; Mismatches 35; Indels 26; Gaps 5; Matches 28; Matches 35; Indels 26; Gaps 5; Matches 28; Matches 28; Matches 35; Indels 26; Gaps 5; Matches 28; Matches 35; Indels 26; Gaps 5; Matches 35; Indels 26; Gaps 5; Matches 28; Matches 35; Indels 26; Matches 28; Matches 29; Matches 28; Matches 29; Matches 2
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                                     seq
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           March 14, 2001, 06:48:04; Search time 62.96 Seconds
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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PCT-US94-01024-5
US-08-082-849B-5
PCT-US94-01024-7
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PCT-US94-01024-7
US-08-081-081-9
PCT-US94-01524-9
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US-08-081-081-3
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6.2	6.2	6.2	6.2	6.2	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6. 5	6.5	6.5	6.5
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Sequence 1, Appli	Sequence 1, Appli	Seguence 1, Appli	Sequence 169, App	Sequence 169, App	Seguence 4, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 14, Appl	Sequence 13, Appl	•	Sequence 25, Appl	Sequence 25, Appl	Sequence 1342, Ap	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-232-463-14/c
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                      TELEFAX: (703)663-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                 APPLICATION NUMBER: US/07/935
FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26 - AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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CITY: Alexandria
STATE: VA
COUNTRY: USA
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Best Local Similarity 5.39 Matches 21; Conservative

5.38;

Pred. No. 3.9e-07; 25; Mismatches 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Patent No. 5231168
; APPLICANT: DZIEGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOREN;
;VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
; TITLE OF INVENTION: MALARIA ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 241; Conserv
                                                                                                                               1440
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                 192 aatteegaaagataaategaaagtggeaggetatattgaaatteeagatgetgatattaa
                                                                                                                                                                                                                                                                                           132 atatgataaaaatgtaaaagaacaggcgagtaaaagataaaagcagcaagctaaacctca 191
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                                                                                                                                                           252 agaaccagtatatccaggaccagcaacacctgaacaattaaatagaggtgtaagctttgc 311
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                                                                                        agaagaaaatgaatcactagatgatcaaaatatttcaattgcaggacacactttcattga 371
                                                                                                                                                                                               aatagtagaggttgaagaaattctaccagaagataaaaatgaaaagttgaacatgaaat 1439
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Pred. No. 6.8e-06;
0; Mismatches 302;
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; LOCATION:
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                               Query Match
Best Local Similarity
Matches 230; Conserv
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APPLICANT: Williamson, Kim (
APPLICANT: Kaslow, David C.
                                                                                                                                                                                                                                                                           TELEFAX: (415)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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84 tatcgataattatcttcacgataaagataaagatgaaaagattgaacaatatgataaaaa 143
                                                                                                                                             NAME/KEY:
                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                           STRANDEDNESS:
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SYSTEM: PC-DOS/MS-DOS
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Center, 8th Floor
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                              Score 50.6; DB 1;
Pred. No. 0.0014;
0; Mismatches 299;
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                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                             SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
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                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                  SEQUENCE CHARACTERISTICS:
                                                                          TELECOMMUNICATION INFORMATION:
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                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REGERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 APPLICATION NUMBER: US/OFFILING DATE: 10-JUL-1996
                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                              STREET: 411 H
                                                TELEFAX:
                                                            TELEPHONE:
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                                                            201-487-5800
                                                                                                                                                                                                             Release #1.0,
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                                                                                                                                                                                                           Sequence 5, Patent No.
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                                                                      APPLICANT: Arora, Naveen
APPLICANT: Singh, Naveen
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS
TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 12
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                                                         CORRESPONDENCE ADDRESS:
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STREET:
CITY: A
STATE:
                                           ADDRESSEE:
              Atlanta
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US-08-021-601-5
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                                                 GENERAL INFORMATION: APPLICANT: Leppla
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APPLICANT:
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LOCATION:
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                                                                                                           Application US/08021601
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           Leppla, Stephen H
Klimpel, Kurt R.
Nichols, Peter J.
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E: Needle & Rosenberg, P.C. 133 Carnegie Way, Suite 400

Nichols, Peter J.

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                                                                    Sequence 5, Application US/08082849B Patent No. 5677274 GENERAL INFORMATION:
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Best Local Similarity 44.9%;
Matches 182; Conservative
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 APPLICANT:
                                     APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                            466 acaagtataagagatgttaagcctacagatgtaggagttctagat 510
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Arora,
Singh,
                                   Leppla, Stephen H
Klimpel, Kurt R.
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Pred. No. 0.0032;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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406 gccaaaaaaggtagtatggtgtactttaaagttggtaatgaaacacgtaagtataaaatg 465
                                     361 GCAAAAGAAGGATATGAACCCGTACTTGTAATCCAATCTTCGGAAGATTATGTAGAAAAT
                                                                                                          301 AAGAAAAAAAAAAAAGACATTTATGGGAAAGATGCTTTATTACATGAACATTATGTATAT
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OTHER INFORMATION:
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                                                                    tcaattgcaggacacactttcattgaccgtccgaactatcaatttacaaatcttaaagca 405
                                                                                                                                         caattaaatagaggtgtaagctttgcagaagaaaatgaatcactagatgatcaaaatatt 345
                                                                                                                                                                                                                                                      AAGCTACTTGAGAAAGTACCATCTGATGTTTTAGAGATGTATAAAGCAATTGGAGGAAAG 240
                                                                                                                                                                                                                                                                                       gataaaaagcagcaagctaaacctcaaattccgaaagataaatcgaaagtggcaggctat 225
                                                                                                                                                                                                                                                                                                                            AAACACATTGTAAAAATAGAAGTAAAAGGGGAGGGAAGCTGTTAAAAAAAGAGGCAGCAGAA 180
                                                                                                                                                                               ATATATATTGTGGATGGTGATATTACAAAACATATATCTTTAGAAGCATTATCTGAAGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFURE 31,677
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Pred. No. 0.0032;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1368;
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PCT-US94-01624-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND TITLE OF INVENTION: RELATED METHODS
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGICAL: DN
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CURRENT APPLICATION DATA:
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NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                        FEATURE
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166 gataaaaagcaagcaagctaaacctcaaattccgaaagataaatcgaaagtggcaggctat 225
                                                  121 AAACACATTGTAAAAATAGAAGTAAAAGGGGGAGGAAGCTGTTAAAAAAAGAGGCAGCAGAA 180
                                                                     106 aaagattaaagatgaaaagattgaacaatatgataaaaatgtaaaagaacaggcgagtaaa 165
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OTHER INFORMATION:
OTHER INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                    Local Similarity
nes 182; Conserv
                                                                                                                                                                                                                                                                                                      ORGANISM:
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                                                                                                                    Conservative
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"LF(1-254)--TR--PE(401-602)"
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                                                                                                                  Score 48.2; DB 4;
Pred. No. 0.0032;
0; Mismatches 223;
                                                                                                                                                 Length 1368;
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US-08-021-601-7
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; LOCATION:
US-08-021-601-7
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GENERAL INFORMATION:
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                                                                                                                                                                  TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn
                                                 MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polania
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                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                     NAME: Spratt, Gwendolyn D
REGISTRATION NUMBER: 36,0
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US FILING DATE: 19930212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 30303
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                                   NAME/KEY:
                                                                                   TOPOLOGY:
                                                                                                                  TYPE: NUCLEIC ACID
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                                                                                                                                    . 1425 base pairs
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133 Carnegie Way, Suite 400
                                                                                                                                                                                       404/688-9880
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Singh, Yogendra
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                                                                 DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                TELEFAX: (4
                                                                  NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31.677
REFERENCE, DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Anthrax Toxin Fusion Proteins TITLE OF INVENTION: Related Methods
SEQUENCE
                                                                                                                                     APPLICATION NUMBER: US 08 FILING DATE: 12-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nichols, Peter J.
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                                                TELEPHONE:
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                APPLICATION NUMBER: US/0: FILING DATE: 25-JUN-1993
                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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nes 182; Conservative
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CHARACTERISTICS:
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             (415) 576-0300
OR SEQ ID NO:
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Singh, Yogendra
                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Francisco
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Op Embarcadero Center, Eighth
                                                    (415)
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; OTHER INFORMATION:
US-08-082-849B-7
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Best Local Similarity
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and ADDRESSEE: TOWNSEND TOWNSEND KHOURIE AND ADD
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TITLE OF INVENTION: ANTHRAX TOXIN FUSION
TITLE OF INVENTION: RELATED METHODS
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MOLECULE TYPE: DN
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                                                                                                                                                                                                                                                        CITY: San Francisco
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                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                               USA
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Singh, Yogendra
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Sequence 9, Application US/08021601
Patent No. 5591631
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Nichols, Peter J.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
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Best Local Similarity 44.9
Matches 182; Conservative
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REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
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ORIGINAL SOURCE:
TITLE
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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ANTHRAX TOXIN FUSION PROTEINS
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"LF(1-254)--TR--PE(398-613)"
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5, 1993
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Pred. No. 0.0032;
0; Mismatches 223;
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US-08-021-601-9
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Best Local Similarity
Matches 182; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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NAME: Spratt, Gwendolyn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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CLASSIFICATION:
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FILING DATE: 19930212
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AGTAAAATTAATCAACCATATCAGAAATTTTTAGATGTATTAAAT 525
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                          acaagtataagagatgttaagcctacagatgtaggagttctagat 510
                                                          ACTGAAAAGGCACTGAACGTTTATTATGAAATAGGTAAGATATTATCAAGGGATATTTTA
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Y: USA
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404/688-9880
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.0033;
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                                                                                                                                                                                                                                                                                     Best Local Similarity
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APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                               286 caattaaatagaggtgtaagctttgcagaagaaaatgaatcactagatgatcaaaatatt 345
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RESULT 13
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APPLICANT:
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ORIGINAL SOURCE:
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                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                MOLECULE TYPE:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                       NAME/KEY:
                                                                                                                                                                      ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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Singh, Yogendra
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                                                                                                                             TELEFAX: 404/688-9880
NFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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                                   MOLECULE TYPE
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                  SOURCE:
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133 Carnegie Way, Suite 400
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Nichols, Peter J.
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Singh, Yogendra
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SYSTEM: PC-DOS/MS-DOS
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Bacillus anthracis
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; FEATURE:
; NAME/KEY:
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US-08-021-601-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Singh, YO
APPLICANT: Nichols,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLF
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                              CLASSIFICATION:
                                                                               FILING DATE:
                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                CITY:
                                                                                           APPLICATION NUMBER:
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N: 514
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; NAME/KEY: CDS
; LOCATION: 580..2907
; OTHER INFORMATION: /product= "Lethal Factor"
US-08-082-849B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.8%;
Best Local Similarity 44.9%;
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
(INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3291 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-161-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
1060 AGTAAAATTAATCAACCATATCAGAAATTTTTAGATGTATTAAAT 1104
                                                                                      1000 ACTGAAAAGGCACTGAACGTTTATTATGAAATAGGTAAGATATTATCAAGGGATATTTTA 1059
                         466 acaagtataagagatgttaagcctacagatgtaggagttctagat 510
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Pred. No. 0.004;
0; Mismatches 223;
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Search completed: March 14, 2001, 14:28:04 Job time: 27600 sec

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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-292-437-2
621
                                                                                         March 14, 2001, 06:46:34; Search time 1314.13 Seconds (without alignments) 2418.424 Million cell updates/sec
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the number of results predicted by	g_pr8	_htg2	hta0	at.	pat1	sts2	qb_sts1:*	pr7:	pr6:	em_htg10:*	htg9	em_htg8:*	ba3:	vi2:	vi1:	htg2	htg22	htg2	htg20	htgl	htg18	hum6:	htg7	htg6	htg5	htg4	htg1	gb_htg16:*	htg1	in3:	htg1	htg1	htg1	htg1	htg1	5	htg8:	pr5	р13	hum	em_htq3:*	۵

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10.0	10.0	10.1	10.1	10.3	10.3	10.3	10.4	10.5	10.7	10.7	10.7	10.8	10.8	10.8	11.0	11.7	50.8	54.8	100.0	Match	Query	٥
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AC024285	CNS05TEB	AF056936	AC013349	AC011856	CNS01JRG	AC021008	AE001373	I66494	A00661	PFRESAR1	AC015927	E08995	E10126	E10125	AC005507	PFMAL1P1	AF269386	AF269739	AF162687	ID		
AC024285 Homo sap			AC013349 Homo sapi			ACO21008 Mus muscu	. AE001373 Plasmodiu	I66494 Sequence 14	A00661 P.falciparu	x05182 P.falciparu	AC015927 Homo sap.	E08995 DNA encodir	E10126 DNA encodir	E10125 DNA encodin	AC005507 Plasmodiu	AL031744 Plasmodiu	AF269386 Staphyloc	AF269739 Staphyloc	AF162687 Staphyloc	Description		

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BASE CO
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AUTHORS
TITLE
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ORGANISM
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Staphylococcus a
AF162687
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                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. 1 (bases 1 to 1256)
Mazmanian, S.K., Liu, G., Ton-That, H. and Schneewin
                                                                                                                                                                                                                                                                                             Submitted (24-JUN-1999) Microbiology Conte Avenue, Los Angeles, CA 90095,
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Mazmanian, S.K., Liu,
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                                                /product="sortase"
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AL110675 Botrytis
AC036177 Homo sapi
AL008970 Plasmodiu
AC015961 Homo sapi
AC022680 Homo sapi
Continuation (2 of
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AC034105 Homo sapi
AC032851 Homo sapi
AC022851 Plasmodium
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                 Kimmerly,W.J., Taylor,J.David, Nelsen,A.J., Godlevski,M.Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller, Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shephe Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller, Furdon,P.J.
                                                                                                                                             Staphylococcus epidermidis.
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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Staphylococcus (
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Research Triangle Park, North Carolina 27709-3398, USA
Location/Qualifiers
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/strain="SR1"
/db_xref="taxon:1282"
/clone="step.1020h12"
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Taylor, J. David, Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, Listenbee, S., Ashanti, C., Shepherd, C., Caro, C., 
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/db_xref="taxon:1282"
/clone="step.1003a02"
/ 647 c 616 g 1/
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On Aug 12,
For more ir
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Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on Aug 12, 1999 this sequence version replaced gi:5706481. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.IMPORTANT: The sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum chromosome 1 strain PROGRESS ***, in unordered pieces. AL031744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contaminated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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Pred. No. 0.0043;
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                                                                                                                                                                    240;
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center, Star
94304, USA
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Submitted (21-AUG-1998) Stanford
Center, Stanford University, 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Kurdi,O.B., Conway,A.B. and Davis,R.W. Plasmodium falciparum 3D7 chromosome 12
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Eukaryota; Alveolata; Apicomplexa;
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Hyman,R.W., Qin,F., Fung,E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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***, 2 unordered pieces.
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/clone="3D7"
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/db_xref="taxon:5833"
/chromosome="12"
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[1-2069]
Doi H., Nagakuchi Y., Tanaka Y., Fujisaki Y.;
Doi H., Nagakuchi Y., Tanaka Y., Fujisaki Y.;
"GENE CLONE MANIFESTING CHICKEN LEUCOCYTOZOON IMMUNOGENIC
RECCOMBINANT VACCINE AGAINST CHICKEN LEUCOCYTOZOON";
Patent number JP1995284392-A/1, 31-CCT-1995.
DOUBUTSUYOU SEIBUTSUGAKUTEKI SEIZAI KYOKAI, KITASATO INST-
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02-SEP-2000
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DOI HIROHITO, NAGAKUCHI YOSHIO, C12N15/09, A61K39/015,C12P21/02;
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/note="EcORI adaptor"
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/product="immunogenicity p
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                                                   /organism="Leucocytozon/strain="shizuoka"
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Best Local Similarity
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                                                                                                              DNA encoding an maltose-binding
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DOI H., Nagakuchi Y., Tanaka Y., "GENE CLONE MANIFESTING CHICKEN
                                                        unidentified unclassified
                                                                                          JP 1995284392-A/2
                                                                                                                                                 08-OCT-1997
02-SEP-2000
                                                                                                                                                                                     E10126.1
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                      1-3399
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, Fujisaki Y.;
LEUCOCYTOZOON
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Query Match
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Matches 237
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DOUBUTSUYOU SEIBUTSUGAKUTEKI SEIZAI KYOKAI, KITASATO
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              aaatgacaagtataagagatgttaagcctacagatgtaggagttctagatgaacaaaaag
                                                                 aagcagccaaaaaaggtagtatggtfactttaaagttggtaatggaaacacggtaagtata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artificial sequences.
JP 1995284392-A/2
31-OCT-1995
19-APR-1994 JP 1994080643
AAGTAACACGTGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAAAAAGAAGTAACAC
                                                                                                     atatttcaattgcaggacacactttcattgaccgtccgaactatcaatttacaaatctta
                                                                                                                                                                                                                                                                                     gtaaagataaaagcagcaagctaaacctcaaattccgaaagataaatcgaaagtggcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         topology: Linear;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:32644"
/organism="unidentified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Artificial"
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                                                                 Query Match
Best Local :
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                                                                                                                                                                     Kato A., Onaga H., Ueda S.;
"POLYPEPTIDE INDUCING IMMUNITY AGAINST LEUCOCYTOZOON RECOMBINANT DNA MOLECULE CODING THE POLYPEPTIDE";
Patent number JP1995089995-A/1, 04-APR-1995.
                                                                                                                                                                                                                                                                                                                                                                    [1]
1-1686
                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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02-SEP-2000
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                                                                                                                                                                                                                                                                                                                            DOUBUTSUYOU SEIBUTSUGAKUTEKI SEIZAI KYOKAI,
                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                      JP 1995089995-A/1.
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ataaaaatgtaaaagaacaggcgagtaaagataaaaagcagcaagctaaacctcaaattc
                                   aaccacatatcgataattatcttcacgataaagataaagatgaaaagattgaacaatatg
                                                                                                                                                                                                                                                                   KATO ATSUSHI, ONAGA HIROSUKE,
C07K14/44,A61K39/015,C12N1/21,
                                                                                                                                                                                                                                                                                           Leucocytozoon caulleryi
JP 1995089995-A/1
04-APR-1995
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                         mat_peptide
                                                                                                                                                                                                           source
                                                                                                                                                                                                                                   topology:
                                                                                                                                                                                                                                            strandedness:
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                                                          245;
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                                                                 Similarity
                                                                                                    1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                          Conservative
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                                                                                                                   /db_xref="taxon:32644"
/organism="unidentified"
                                                                                                   915 A; 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52,
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                                                                                                                                                                  /organism="Leucocytozoon c
/note="mRNA is derived fro
1. 1686
/product="a protein involv
phylaxis"
                                                                  10.8%;
45.2%;
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JOURNAL
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ORGANISM
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AC015927/c
LOCUS
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                Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6939328.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria: Primates; Catarrhin1: Hominidae; Homo. 1 (bases 1 to 131271)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Homo sapiens chromosome
SEQUENCE SAMPLING.
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* 8178 8277; gap of 100 bp

* 8278 9219; contig of 917 bp .

* 8278 9219; contig of 942 bp in 10288; contig of 969 bp in 10288; contig of 969 bp in 10289 10388; gap of 100 bp in 11289 11388; gap of 100 bp in 1289 11388; gap of 100 bp in 1289 11388; gap of 100 bp in 12314; contig of 926 bp in 12315; contig of 926 bp in 13357 13456; contig of 626 bp in 13357 1345
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                                                                                                                                                    19535: gap of 100 bp
19636 20548: contig of 913 bp
20549 20648: gap of 100 bp
20649 21589: contig of 941 bp
21590 21689: gap of 100 bp
21590 22598: contig of 909 bp i
22599 22698: gap of 100 bp
22599 23638: contig of 940 bp i
23639 23738: gap of
                                                                         24667: conti.
24668 24767: gam - 1
24768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13457 14399: contig of 943 bp
14400 14499: gap of 100 bp
14500 15459: contig of 960 bb
15460 15559: gap of 100 bp
15560 16453: contig of 894 bp
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7261 8177: contin ~f ~ 8178 8777
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3984: contig of 928 bp
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5 5036: conti
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                                     25782: gap of 26715: contig
                        26815:
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                                                                      4/67: gap of 25682:
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18538: con+
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27865:

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1227 41326: gap of 100 t
1327 42275: contig of 949
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9 63968: contig of 9
9 64068: gap of 10
9 64986: contig of 9
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2 44336: contig of 9
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48460: contig of 936 bp
4850: gap of 100 bp
49507: contig of 947 bp
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40231: contig of 951 bp
40331: gap of 100 bp
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56781: contig of
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55741: contig of
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52631: contig of
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62918: contig of 918
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54720: contig of
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RESA mRNA

for ring-infected eryrthrocyte

6-FEB-1998

ACCESSION VERSION

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                                                                                                               ACATGATGCTGAAGAAATGTAGAACATGATGCTGAAGAAAATGTAGAAGAAATGTTGA
Data kindly reviewed (10-JUL-1987) by Favaloro For FC27 RESA genomic sequence see X04572; for sequence see X05181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COWMMAD, A.F., Coppei, R.L., Saint, R.B., Favaloro, J., Crewther, P Stahl, H.D., Bianco, A.E., Brown, G. V., Anders, R.F. and Kemp, D.J. The ring-infected erythrocyte surface antigen (RESA) polypept. Plasmodium falciparum contains two separate blocks of tandem
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/translation="NSITYNFENINSNVDNGNQSKNISDLSYTDQKEILEKIVSYIVD
ISLYDIENTALNAAEQLLSDNSVDEKTLKKRAQSLKKLSSIMERYAGGKRNDKKSKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ring-infected eryrthrocyte surface antigen"
/protein_id="CAA28817.1"
/db_xref="GI:1335718"
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/clone="FC27 Ag46"
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VLNQIAWKALSNQIQYSGRKIMNSDISSFKINELKSLEHRAKAKAAEAEMKKRAQKPK
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TVKDGVYLDHETSDALYTDEDLLFDLEKQKYMDMLDTSEEESVEENEEEHTVDDEHVE
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EFNPLLVDKVLFDYNEKVDNLGRSGGDIIKKMQTLMDEIMDINKRKYDSLKEKLQKTY
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/db_xref="taxon:5833"
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/protein_id="CAA00077.1"
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        tggtaatgaaacacgtaagtataaaatgacaagtataagagatgttaagcctacagatgt
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence.
AE001373 AE001362
AE001373.1 GI:384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erratum:[[published 4;282(5395):1827]]
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HDIDETDYYIGSILGYSDFMNKMKYQNTQIDNNKGKKTTNTMEKNKKNDKKHSKHSKKNK
TKQNYKYKKENQNIEMHIPQSKYKQERIEILDDNGKELKSHKNIKEEKGGIEKTDTTN
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6675. .10253
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                                                                                                                                                                                      /note="predicted
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                                                                                                                                                                                                        /gene="PFB0115w"
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Query Match
Best Local Similarity
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Lander, E
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AUTHORS
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209

7669

QΥ 망 QΥ

149

7609

ORIGIN BASE COUNT

Matches

89

Riven, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Roderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, G., Liu, G., Locke, K., Macdonald, P., Marguis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Schole, R., Schol Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Direct Submission Mus musculus chromosome 11, clone RP23-59C1 (bases and Zody, M. 1 to 201289) Genome

Submitted (12-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2000 this sequence version replaced gi:8980920. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center project name: L573 Center clone name: 59_C_1 Contact: sequence_submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu Center code: WIBR Center: Whitehead -- Genome Center Project Information Institute/ MIT Center for Genome Research L5731

* NOTE: This record contains 226 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced. * However, it should not be assumed that this clone will be sequenced to completion. In the event that the record preserved. 100 bp 5628: contig of 717 b, 5629 5728: gap of 100 bp 5729 6452: conti 1 702: contig of 702 bp in length
703 802: gap of 100 bp
803 1492: contig of 600 bp in length
1493 1592: gap of 100 bp
1593 2324: contig of 732 bp in length
2325 2424: gap of 100 bp 9699: contig of 710 bp in 100 9799: gap of 100 bp 1 10(3980: contig of 7 %1 4080: gap of 100 1 4811: contic 100 bp 3157: contig of 733 b 3257: gap of 100 b 4011: contig of 731 4911: gap of 100 bp 5628: contin 1 6552: gap of 7276: con 8196: 7376: is updated, the accession number will 8096: gap of i: contig of 720 bp of 100 bp contig of 724 bp in contig 100 bp 3 of 693 b 100 bp of 724 b 100 bp of 723 bp in length 100 bp dq ďď þp bp in length bp in length Ín 'n in Length length length length length

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389

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Вþ

8029

REFERENCE AUTHORS

SOURCE ORGANISM

KEYWORDS ACCESSION VERSION

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38029: gap of 100 bp
38740: contig of 711 bp
38840: gap of 100 bp
39549: contig of 709 bp
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66 51870: contig of 705 bp in

151670: gap of 100 bp

1 52408: contig of 738 bp in

1 52508: gap of 100 bp

3 5318: contig of 739 bp in

5318: contig of 739 bp in

5318: contig of 677 bp in

53285: gap of 100 bp

54103: gap of 110 bp
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15 54914: gap of 729 b

16 55643: contig of 729 b

17 56475: contig of 732 b

18 56475: gap of 100 bp

19 56575: gap of 704 b
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25893:

26593

contig of

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93: contig of gap of

6 33975: gap of 10 34649: contig of 6 0 34749: gap of 10 0 35466: contig of 7 7 35566: gap of 10 36288: contig of 7

100

33171: gap of 33875: contig of 32269: contig of 32369: gap of 33071: contig of

31550:

31450:

100 bp

36388: gap of 37121: con

contig of

100

37221:

21: gap of 37929: contig of

549: gap of 40340: con

11 17830: gap of 10 11 18512: contig of 6 13 18512: gap of 10 13 19313: contig of 7 14 19413: gap of 10 14 19413: gap of 10

682

17057: gap of 17730: contig of

673

15437: gap of 16151: contig of

16251:

con :: gap of 16957:

contig of

13023: gap of 13737: contig of

13837:

14647:

17: gap of 15337: contig of 37: gap of 14547: contig of

690

710

12211: gap of 12923: contig of

11303: contig of 719 11403: gap of 100 P

03: gap of 12111: contig of

2 20151: gap of 10 2 20872: contig of 1 3 20972: gap of 1 3 21700: contig of 7 1 21800: gap of 1 1 22526: contig of 7

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                                                             gaccagcaacacctgaacaattaaattagaggtgtaagctttgcagaagaaaatgaatcac 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cnsUlJRG 879 bp DNA STS 17-FEB-2000 Anopheles gambiae STS T7 end of clone 14007 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito), sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is from an A. gambiae BAC library provided by F.H Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Culicidae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roux, Paris 75015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles gambiae
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/note="end : T7"
38 c 1 g 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="14D07"
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Search completed: March 14, 2001, 14:30:10 Job time: 27816 sec

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1228 epb_estf():*
1229 epb
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
CNS018GS/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

CNS018GS 942 bp DNA GSS 26-JUL-1999
TION Drosophila melanogaster genome survey sequence T7 end of BAC
BACN13P09 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
TON AL109318
N AL109318.1 GI:5629622
DS GSS.

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CNS00880 593 bp DNA GSS 03-JUN-19
Drosophila melanogaster genome survey sequence TET3 end of
BACR16J23 of RPCI-98 library from Drosophila melanogaster (
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly.
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/plasmid="pBeloBACI1"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN13P09"
/note="end : T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual mar clanes the entire library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can l found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web : www.genoscope.cns.fr)Determination of this BAC-end sequence was carried out
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BP 191 91006 EVRY cedex
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR16J23"
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- FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University
100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          894 bp mRNA EST 25-JUL-2000 HV_CEb0006H11f Hordeum vulgare seedling green leaf EST library HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA HV_CEb0006H11f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wing RA Clemson University Genomics Institute
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y.
Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,Y., Anderson,H., Dale,J., Simmons,J., Choi,D.W., Main,D. and
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/note="Vector: lambdaZAP;
/note="Vector 41 g 85
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/clone=lib="Hordeum vulgare seedling
/tlorary HYCDNA0005 (Erysiphe infected
/tissue_type="seedling green leaf"
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/cultivar="CI16151 (Mla6)"
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                                                                                                                                                                                                                                                         d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector {\bf r}
                                                                                                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Bilaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL102403
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                                                                                                           /clone_lib="DrosBAC"
/clone="BACN09C07"
/note="end : SP6"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Tetraodon nigroviridis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
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                                                         Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part o scale clone-end sequencing project of the Tetraodon nigrov genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon
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Roest-Crollius, H.,
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/organism≖"Tetraodon nigroviridis"
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- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila
                                                                                                             Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                            fly), genomic survey s
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                                                                                                                                                              Drosophila melanogaster genome survey sequence TET3 end of BAC BACR13F18 of RPCI-98 library from Drosophila melanogaster (fruifly), genomic survey sequence.
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                                                                                                              GSS.
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                                                                                        fruit fly.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR35J09"
/note="end : T7"
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Mismatches 233; Indels
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GKKAAAAAAAAAAAKGGWAAAAAAAAAAAKAKTAAAT
                                                                         RAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAKKDAKAKKTKAAAAAAGAGATADAGADGK
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                                                                                                            gtaaagataaacaattaacattaattacttgtgatgattacaatgaaaagacaggcgttt
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Direct Sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration with the Berkeley Drosophila Genome Project (BDGP) The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Web : www.genoscope.cns.fr)
Determination of this BAC-end
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/note="end : TET3"
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                              ccgaactatcaatttacaaatcttaaagcagccaaaaaaaggtagtatggtgtactttaaa 435
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC End Sequences at ATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jecker@atgenome.bio.upenn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T24D11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: HindIII;
; Produced by Rod Wing"
50 c 53 g 678 t 372 others
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ccagcaacacctgaacaattaaatagaggtgtaagctttgcagaagaaaatgaatcacta 330
                                   ARAAWWWATGGAGTAAWAAAWATWTAAWRTTTTAAGAAAAAAAAAWWGTWGGAWWARAWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome survey sequence SP6 end BACN37M13 of DrosBAC library from Drosophila melanogast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               project grant. The DNA was and Genevieve Payan. It has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN37M13"
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Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
                                                                                                                                                                                                                                                                                                                                                                                               d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/clone="BACN12N03"
/note="end : T7"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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2 (bases 1 to 1135)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ dat
This sequence is a single read and was generated as
scale clone-end sequencing project of the Tetraodon
genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasil Bouneau, L., Billault, A., Quetier, F., Weissenbach, J.
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clo
208P24 of library G from Tetraodon nigroviridis, genomic survey
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                                                     http://www.genoscope.cns.fr/Tetraodon
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/organism="Tetraodon nigroviridis"
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                                                 A BĀC End Sequencing Framework to Sequencing by Depublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
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nbxb0046J18r CUGI
          Tel:
Fax:
                              Clemson University
100 Jordan Hall, C
                                                                                                                                      Oryza sativa.
Oryza sativa
                                                                                            Wing, R.A. and Dean, R.A.
                                                                                                        Magnoliophyta; Liliopsida;
1 (bases 1 to 870)
                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
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/clone="208P24"
/clone_lib="G"
/note="Genoscope sequence ID : COAG208DH12SP1~end
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
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/strain="Japonica"
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/lab_host="E. coli DH10B"
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AAAAATAATATAAAAAAAATAATAWAWAAAAAATTAAWTATCAANNCACANTCTTCNCNA
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
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/clone="BACN37F07"
/note="end : SP6"
a 70 c 85 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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segref@genoscope.cns.fr
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                                                              aagataaaaagcagcaagctaaacctcaaattccgaaagataaatcgaaaagtggcaggct 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 3134 row: M column: 12
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HS_3134_A2_G06_T7C CIT Approved Human Genomic Sperm
sapiens genomic clone Plate=3134 Col=12 Row=M, DNA s
AQ897460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ897460.1 GI:6353650 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC,
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector:
E-Coli DH10B"
a 20 c 110 g 32 t
                                                                                                                                                                                                                                                                                                              /clone="Plate=3134 Col=12 Row=M"
/clone_lib="CIT Approved Human G
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                  /sex="male"
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Primates;
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Pred. No. 4.6e-05;
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                                                                                                                                                                                                                                         Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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                                                                                                                                                                                                      and how to order individual BAC clones, the entire filters for hybridization from the BACPAC Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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               /organism="Drosophila n
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR17J10"
/note="end: T7"
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p30189 drosophila
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Vitadello M., Vettore S., Lamar E., Chien K.R., Gorza L.;

"Neurofilament M mrNA is expressed in conduction system myocytes of the developing and adult rabbit heart.";

J. Mol. Cell. Cardiol. 28:1833-1844(1996).

-i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

-i- PTM: THERRE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
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01-OCT-1996 (Rel. 34,
01-OCT-2000 (Rel. 40,
NEUROFILAMENT TRIPLET
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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(NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M) (FRAGMENT).
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Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown [Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., I Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D. Rajandream M.A., Ries E., Rowley N., Skelton J., Smith V. Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
PFAM; PF00270; DEAD; 1.
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PF000271; helicase_C; 1.
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"Identification of six phosphorylation
tail region of the rat neurofilament pr
J. Biol. Chem. 267:4467-4471(1992).
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Mapolitano E.W., Chin S.S.M., Colman D.R.,
"Complete amino acid sequence and in vitro
the middle molecular weight neurofilament
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01-MAY-1992 (Rel. 22,
01-OCT-2000 (Rel. 40,
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                        entities requires a
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01-OCT-2000 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT MEDIUM POLYPEPTIDE) (NF-M).
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SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                  PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NEM PHOSPHORYLATED ON A NUMBER OF THE SERIMES IN THIS MOTIF: IT IS THOUGHT THAT PHOSPHORYLATION OF THE RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANG
                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 268:16679-16687(1993).

FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, MAINTENANCE OF NEURONAL CALIBER.
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license@isb-sib.ch).
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               Noback M.A., Terpstra P., Holsappel S., Ve
"A 22 kb DNA sequence in the cspB-glpPFKD
Bacillus subtilis chromosome.";
Microbiology 142:3021-3026(1996).
                                                                                        Bacillus subtilis.
Bacteria; Firmicutes;
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                                        Noback M.A.,
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         or
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                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Amphibia; Batrachia; Anura; Mesobatrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
TRANSMEM 7 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                      entities
                                                                                              This
                                                                                                                                                                                                                                                                      condensation in vitro.";
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P50532;
01-0CT-1996
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                                                                                                                                                                                                                                                                                                   Hirano T., Mitchison
                                                                                                                                                                                                                                                                                                                MEDLINE=95042742;
                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                      XCAP-C
                                                                                                                                                                                                                                                                                    "A heterodimeric coiled-coil protein required for mitotic chromosome
                                                                                                                                                                                                                                                                                                                                                          Kenopodinae;
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                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES. DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS PLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
                                                European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                        SIMILARITY: BELONGS TO THE SMC FAMILY
                                                                                                                                                                                                             MITOTIC CHROMOSOMES.
SUBUNIT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERODIMER
                                                                                                                                                                                                                                        FUNCTION: REQUIRED FOR BOTH ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                              SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                       79:449-458(1994)
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         an
                         non-profit institutions as rony and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                      requires
                                                                                                                                                                                                                                                                                                                                                                                                                            96 (Rel. 34, Created)
16 (Rel. 34, Last sequence up
18 (Rel. 36, Last annotation
ASSEMBLY PROTEIN XCAP-C
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       to license@isb-sib.ch).
                      a license agreement
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21976 MW;
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Pred. No. 1.8;
33; Mismatches
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                      (See http://www.isb-sib.ch/announce,
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There are no restrictions
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SEQUENCE
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DOMATN
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                                                                                neurofilaments.";

Proc. Natl. Acad. Sci. U.S.A. 85:1998-2002(1988).

-:- FUNCTION: NBUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L,

-:- EUNCTION: NBUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L,

-:- END H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBE!

-:- PTM: THERE ARE A NUMBER OF REPEARS OF THE TRIPEPTIDE K-S-P, NFI

PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS

THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
                                                                                                                                                                                                                                                             sequence and the relationship of its filament gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                               MEDLINE=88158120;
                                                                                                                                                                                                                                                                                     Myers M.W., Lazzarini R.A., Lee V.M.-Y., So
"The human mid-size neurofilament subunit:
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    Mammaila;
                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P07197;
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                                                                                                                                                                                      Lee V.M.-Y., Ot
Lazzarini R.A.;
                                                                                                                                                                                                                                                                                                            MEDLINE=87275853;
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                        'Identification of the major multiphosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 NREKFTQLDLQDVDTREKLKHSKSKVKKLQK--QLQKDKEKVDELKNVPANSQKIIAEET 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 YLHD-----KDKD---EKIEQYDKNVKEQA----SKDKKQQAKPQIPKDKSKVAGYIE-
         PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FOR THE LARGER NEUROFILAMENT POLYPETIDES (NE'M AND NF'H) LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                            INTERFILAMENT CROSS OF AXONAL CALIBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRD-VKPTDVGVLDEQKGKDKQLTLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                t gene family.";
6:1617-1626(1987).
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                                                                                                                                                                                                             ONE OF THE 13 RESIDUE REPEATS 58120; PubMed=2450354;
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rini R.A., Lee V.M.-Y.,
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                                                                        BRIDGES THAT ARE IMPORTANT
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                                                                                                                                                                                               Carden M.J., Hollosi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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Catarrhini; Hominidae
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                                 NF-H),
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Best Local (
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                                                                                                               UI-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE)
(PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).
FPR3 OR NETIC CO.
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CARBOHYD
SEQUENCE
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          MEDLINE=95050937; PubMed=7525596;
Benton B.M., Zang J.-H., Thorner J.;
"A novel FK506- and rapamycin-binding
                                           SEQUENCE FROM N.A. STRAIN=YNN 214;
                                                                                     FPR3 OR NPI46 OR YML074C.
Saccharomyces cerevisiae (Baker's
Eukaryota; Fungi; Ascomycota; Sacc
                                                                                                                                                                                                              YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation; Glycoprotein. INIT_MET 0 0
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                                                                           Saccharomycetaceae;
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A27864; A27864.
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J. Biol. Chem. 272:12961-12967(1997).
-i- FUNCTION: PPIASES ACCELERATE THE FOLDING RAPAMYCIN-BINDING PROTEIN. SPECIFICALLY B SEQUENCES. MAY BE INVOLVED IN THE ASSEMBL
                                                                                                                                                                                                                                                                                                                                               This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              located in the nucleolus
J. Cell Biol. 126:853-86;
[3]
                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Purification of FKBP-70, a cerevisiae, and cloning of i
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"Yeast NPI46 encodes a no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97294697;
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                                                                                                                                                                                           BL; L34569; AAB04165.1;
BL; X79379; CAAS5924.1;
BL; S73876; AAB31995.1;
BL; Z46373; CAA86504.1;
R; S47927; S47927;
R; S47927; S47927.
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; S0004539; NPI46.
ERPRO; IPR001179; -
M; PF00254; FKBP; 1
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ENZYME REGULATION: INHIBITED BY BOTH
SUBCELLULAR LOCATION: NUCLEAR; NUCLEO
                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
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PS00454; FKBP_PPIASE_2; 1.
PS50059; FKBP_PPIASE_3; 1.
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(OCT-1994) to
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                                                                                                     Rotamase;
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EMBL/GenBank/DDBJ databases
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                                                     protein; Phosphorylation.
ASP/GLU-RICH (HIGHLY ACIDIC).
LYS-RICH (HIGHLY BASIC).
ASP/GLU-RICH (HIGHLY ACIDIC).
ASP/GLU-RICH (HIGHLY ACIDIC).
                                  LYS-RICH (HIGHLY BASIC).
NUCLEAR LOCALIZATION SIGNAL
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                                     INTERPRO; IPRO02569; INTERPRO; IPRO02579; PFAM; PF01641; DUF25; PFAM; PF01625; PMSR; 1
                                                                                                                                    TIGR;
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"INCUTION: COULD HAVE AN IMPORTANT FUNCTION AS A REPAIR ENZYME PROTEINS THAT HAVE BEEN INACTIVATED BY OXIDATION. CATALYZES TH REVERSIBLE OXIDATION REDUCTION OF METHIONINE SULFOXIDE IN PROTEINS TO METHIONINE (BY SIMILARITY).

"IT SIMILARITY: TO OTHER BACTERIAL AND EUKARYOTIC PEPTIDE METHIONI
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE
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STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=92
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Bacteria; Proteobacteria; epsilon subdivisi
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                                                                                                                                  AE000542; AAD07291.1; HP0224; -.
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                                                                                                                                                                                            non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                 ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                  mitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SURF6 FAMILY.
                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
KLKEMKVERKGKGPAKVTSAMAEKMAEEKRLKRRESKLKLKQRRA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Levy E., Liem R.K.H., D'Eustachio P., Cowan N.J.;
"Structure and evolutionary origin of the gene encoding
the middle-molecular-mass neurofilament protein.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER. PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPILDE K-S-P, NFM IS PHOSPHORVLATED ON A NUMBER OF THE SERINES IN THIS MOTIF IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S00030; S00030.
MGI:97314; NFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration seen the Swiss Institute of Bioinformatics and the EMBL outstation of the Swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and the EMBL outstation of the swiss Institute of Bioinformatics and Bioi
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COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2A.
LINKER 2.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                     repeat pattern; Coiled coil; Neurone;
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DP QA

1840

9

Query Match Best Local S Matches 48

Similarity 48; Conser

Conservative

8.1%;

Score 87; DB Pred. No. 67; Mismatches

79;

72;

Gaps -- 53 Length 2077;

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RESULT 12
TEGU_HSV6U
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Matches 41
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                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; X83413; CAA58411.1; SEQUENCE 2077 AA; 2399.
                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                  Gompels U.A., Nicholas J., Lawrence G., Jones M., Th
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A
"The DNA sequence of human herpesvirus-6: structure,
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=95266321; PubMed=7747482;
                                                                                                                                                                                                                                                                                                                   U31 OR HHRF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                               Virology 209:29-51(1995).
                                                                                                                                                                                                                                                                                         Herpes simplex virus (type 6 / Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                        and genome evolution."
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                                                                                                                            SIMILARITY: BELONGS TO FAMILY 1
EHV-1 24, EBV BPLF1, HVS-1 64,
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Pred. No. 19;
Pred. No. 19;
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O-LINKED
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QA -> RR (IN REF. 2).
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\ stage;
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C1CA4BDC26650511 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PEQLNRGVSFAEENESLDD-----
                                                                                                                                      THAT GROUPS TOGETHER HSV-1 UL36, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                          on update)
                                                                                                                                                                                                                                                                                                                                                                                              2077
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Herpesviridae;
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There are no restrictions on ong as its content is in no
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SIMILARITY).
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J. Cell Biol. 134:923-934(1996).

J. Cell Biol. 134:923-934(1996).

FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

I. CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.

II CAN RELAX BOTH NESCRILLS EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NESCRILANEOUS: EUKARYOTIC SUPERCOILS, WHEERAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.

II SUPERCO
                                      EMBL; M74557; AAA28951.1;
EMBL; U80064; AAC24158.1;
PIR; S35521; S35521.
                                                                                                                                                                                                                                                                                 modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96354910; PubMed=8769417;
Zhang C.X., Lee M.P., Chen A.D., Brown S.D., Hsieh T.-S.;
"Isolation and characterization of a Drosophila gene essential
early embryonic development and formation of cortical cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93117086; PubMed=1335568;
Hsieh T.-S., Brown S.D., Huang P., Fostel
"Isolation and characterization of a gene
T in Drosonhila melanomaster.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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01-OCT-2000 (Rel.
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APR-1993 (Rel. 25, Last sequence up
OCT-2000 (Rel. 40, Last annotation
TOPOISOMERASE I (EC 5.99.1.2)
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                                                                                                                                                                 P11387;
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                                        TOPOISOMERASE_I_EUK;
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            DNA-binding
                                                                                                                                                                                                                                                                                                             agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! J.;
encoding
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                                                                                                                                                                                                                                                                                                                                       Usage
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65 IPKDKSKVAGYIE-----IPDAD--IKEPVYPG-PATPEQLNR-GVSFAEENESLDDQNI 115

Query Match Best Local S Matches 44

1 Similarity 28.4 44; Conservative

7.98;

21;

Score 84.5; D Pred. No. 5.7; 21; Mismatches

DB 1;

Length 195; Indels

55;

35;

Gaps

10;

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RESULT 14
YACE_BRELA
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Best Local Similarity
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DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                               YACE_B
P56187
          Hypothetical protein;
NP_BIND 8 15
NON_TER 195 195
                                                                                     EMBL; L18875; -; NO HSSP; P06143; 1HEY
                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                               Unpublished observations
                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 13869;
                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
HYPOTHETICAL PROTEIN IN PTSG 3'REGION (FRAG
 SEQUENCE
                                                PFAM; PF01121; UPF0038; 1.
PROSITE; PS01294; UPF0038;
                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                            [NTERPRO;
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                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE UPF0038
                                                                                                                                                                                                                                                         X. 图.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-PVY-----PGPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAK 137
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                                                                         IPR001977;
                                                                                                                                                                                                                                                                                            (NOV-1993)
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40
930
972 AA;
195
195 i
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 AA;
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                                                                                                  NOT_ANNOTATED_CDS
           15
195
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198 SER-RICH.
930 DNA CLEAVAGE (BY SIMILARITY).
111688 MW; 3764BBBDEEFA3OCD CRC64;
21135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%;
22.7%;
                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                       ATP-binding
                                                                                                                                                                                                                                           (JAN-1997).
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
D7F0333860E0BDD3 CRC64;
                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 AA
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(FRAGMENT).
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38;
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Query Match
Best Local Similarity
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PS4397;

D1-OCT-1996 (Rel. 34, Created)

O1-OCT-1996 (Rel. 34, Last sequence update)

15.-UUL-1999 (Rel. 38, Last annotation update)

39 KDA FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8).

FK506-BP1 OR FKBP39.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theopold U., Dal Zotto L., Hultmark D.;
"FKBP39, a Drosophila member of a family of proteins that bind
immunosuppressive drug FK506.";
Gene 156:247-251(1995).

-I- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. FKBP5
MAY FUNCTION IN A SIGNAL TRANSDUCTION CASCADE DURING EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                     SEQUENCE
                                                                                                                                                                                                                                            PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG PROSITE; PS00454; FKBP_PPIASE_2; 1. PROSITE; PS50059; FKBP_PPIASE_3; 1.
                                                                                                                                                                                                                                                                                                                                                    FLYBASE; FBgn0013269; FK506-bp1. INTERPRO; IPR001179; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                     Isomerase;
                                                                                                                               DOMAIN
                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH HIGHEST EXPRESSION IN EARLY EMBRYO.
SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED, HIGHEST LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: CIS-TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: EXPRESSED DURING ALL STAGES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                               PF00254; FKBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit
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186
                                                                                                  ΑA;
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183
247
                                                                                                  39428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     institutions as long as its content
7.98;
27.68;
                                                                                                                                                                                                                          Nuclear
                                                                                                  MW.
                                                                                             IT PROTEIN.

ASP/GLU-RICH (HIGHLY ACIDIO
ASP/GLU-RICH (HIGHLY ACIDIO
LYS-RICH (BASIC).

PPIASE, FKBP-TYPE.

W; F12C6431D4C3B55F CRC64;
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Score 84.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
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                       DB
                          <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
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                       Length 357;
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В
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                                                  257
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                                                                                                    200
305 VIKGWDVGVAGMKVGGKR---VITC
                                                                                                                              47
                                                                                                                    KNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPAT--PEQLNRGVSFA 104
                      DVKPTDVGVLDEQKGKDKQLTLITC
                                                                                                   KSGKEQNGVAKKEEAKQQ-QKKKEKPEAKKEQPKA--KEPAKQQPASKDPRTITGGVKIV 256
                                                  DQVVGKGEEAKQGKRVSV---YYIGRLQSNNKTFDSLLKGKPFKFALGGG---
                                                                         EE----NESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIR 159
                                                                                                                                                       40;
                                                                                                                                                       Conservative
                                                                                                                                                       18;
326
                       184
                                                                                                                                                       Mismatches
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                                                                                                                                                       Indels
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Search completed: March 2, 2001, 10:24:33 Job time: 120 sec

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Result
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Perfect score:
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 length: 0
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Gapop 10.0 , Gapext 0.5
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RESULT 2
T25593
T25593
hypothetical protein C32E12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
C;Accession: T25593
R;Wilcox, L.

15-Oct-1999 #text_change 15-Oct-1999

submitted to the EMBL Data Library, November 1996 A;Description: The sequence of C. elegans cosmid C32E12. A;Reference number: Z20055 A;Accession: T25593

A;Status: preliminary; translated from GB/EMBL/DDBJ

Оу Оъ	Оy	ОУ	Qу	Que Bes Mai	RESULT 1 736719 probable i C;Species: C;Date: 03 C;Accessio R;Murphy submitted A;Referenc A;Accessio A;Status: A;Molecule A;Residues A;Cross-ree A;Experime C;Genetics A;Gene: SC		
177 313	124 255	73 195	13 148	Query Ma Best Loo Matches	RESULT 1 736719 probable integ C;Species: Str C;Date: 03-Dec C;Accession: T R;Murphy, L; submitted to t A;Reference nu A;Accession: T A;Status: prel A;Molecule typ A;Residues: 1 A;Reference A;Experimental C;Genetics: A;Gene: SCOEDB		0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
KQLTLITC-DDYNEKTGVWEK : : :: RYITLTTCTPEFTSKYRMIVWGK	DRPNYQFTNLK ::: HGEPFRYIN	AGY IE: : : QGFALLH:	GVVLILVAAYLFAKPHIDNYL 	Match Local Simil	Stre Stre -DecDecT3 L.; H1 to th to th ri T3 preli rype : 1-3 feren feren ntal ntal ntal		87 88 87 87 87 88 87 88 87 88 87 88 87 88 87 88 87 88 87 88 85 88 85 85 86 85 85 86 85 85 86 85 85 86 85 85 86 85 85 85 85 85 85 85 85 85 85 85 85 85
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KTGV 	KGSMVY : PGDPIV	EPVYPG : VPIAEG	(PHIDNY ;; TNVRAH	9. 23. tive	pro eelio ncelio Bent Lil Lil		1291 464 605 712 1199 1909 1909 1909 1909 1909 1909 19
-VWEK	VE3	PAT	1D	28;	protein licolor ce_revi. entley, Library Librard: slated: slated:		2222222222222
196 335	DRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDV- :::	IEIPDADIKEPVYPGPATPEOLNRGV- : : : : : : LHIPKLDVVVPIAEGISSKKVLDRGMV	KDKDEKIEG ;	Score 104; Pred. No. 0; Mismatc	n - r isi isi y, s y, fr	ALIGNMENTS	T22382 T35943 T02350 T02350 T02350 T24782 T24592 T25713 C82901 T22897 T722897 T722897 T722897 T722897 T726718 T736718 T736718 T736718 T736718
	AAKKGSMVYFKVGNETRKYKMTSIRDV-KPTDVGVLDEQKGKD 	VYPGPATPEOLNRGVSFABENESLDDQNISIAGHTFI :	GVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKV :::	re 104; DB 2; Length d. No. 0.61; Mismatches 82; Inde	Streptomyces coelicolor on 03-Dec-1999 #text_cha .D.; Parkhill, J.; Barre June 1999 om GB/EMBL/DDBJ	ENTS	
)EQKGKD PVPKQSGFKGPG	NISIAGHTE : AGNEGLAGHRN	AKPQIPKDKSKV PGSFEPG	352; ls 34;	nge 03- 11, B.G		hypothetical prote probable hydrolyti hypothetical prote outer membrane pro hypothetical protein required protein for the protein for the hypothetical protein hypothetical prote
	D 176 G 312	I 123 II 254	V 72 G 194	Gaps 11;	Dec-1999 .; Rajandream SCOEDB:SCH69.		thetical prote able hydrolyti thetical prote r membrane pro thetical prote r stage antige ment protein thetical protein thetical protein thetical prote thetical protein protein protein larger all forbinding 39k NS-1 protein

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RESULT
A54514
glutamic acid-rich protein precursor
N;Alternate names: GARP
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y48C3A.a - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te: C:Accession: T31583
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A;Cross-references: EMBL:AL117203; NID:e1549827;
A;Experimental source: clone Y48C3A
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A; Introns: 5/2;
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A;Residues: 1-552 <WIL>
A;Residues: 1-552 <WIL>
A;Cross-references: EMBL:U80032; PIDN:AAB53878.1; GSPDB:GN00019;
A;Experimental source: strain Bristol N2; clone C32E12
                                                                                                              g
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A; Introns:
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A; Residues: 1-1089 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z21046
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Best Local S
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                                                                                                                                                                                                                                     KKCSTLLPKIGQVVLIVTDLLIPLEVEEHHLDHDNDLHPPTPSIEEEDDPDDKSSPLPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APKRSKGETQELNQLLENNAQNKPKKVKEPSGIDAIDLKSDSLVVEKTQLSGDSALRVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKPKDKKSKEKKPKAAKSKEVKSKDVKPKDVKSKDEKKKKKNSKGKKPSTDPLFSGPLTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKPHIDNYLHDKDKDE----KIEQYD-----KNVKEQASKD------KKQQAKP 63
                                                                                                             KDPVVPEPMDFGKIQLPERRTREYLSRKAKLAEKN 1036
                                                                                                                                          KEPVYPGP-----ATPEQLNRGVSFAEEN 107
                                                                                                                                                                        PSPAHIQQLPSNLAPKLSQTKAQEAKNSNDTNIQNLSRDINVPRDTNKHQTEVEDCYAEY 1001
                                                                                                                                                                                                       ---- TEQYDKNVKEQASKDKKQQAKP---
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                                parasite
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RESULT S59777
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C:Superfamily: unassigned ribonucleoprotein
F:3-84/Domain: ribonucleoprotein repeat home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, July 1995 A; Description: The sequence of S. cerevisiae A; Reference number: S59764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein YPR112c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P8283.19
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
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A; Residues: 1-887 <NEL>
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C; Superfamily: histone
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A; Residues: 1-678 <TRI>
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A; Accession: A54514
                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Nelson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: tandem
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 EQKGKDKQ 178
                               NNKDEAPNLVIENESDDEYSAL ----
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homology <RRM2>
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A;Cross-references: EMBL:X79743
A;Cross-references: EMBL:X79743
A;Note: the nucleotide sequence was submitted to the EM A;Note: the nucleotide sequence was submitted to the EM C:Genetics:
A;Map position: 9R
C;Superfamily: unassigned DEAD/H box helicases; DEAD/H
C;Keywords: APP: P-loop
F;107-610/Domain: DEAD/H box helicase homology <DEAD>
F;107-114/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurofilament protein M - rabbit (fragment)
()Species: Oryctolagus cuniculus (domestic rabbit)
()Species: Oryctolagus cuniculus (domestic rabbit)
()Date: 15-Jul-1995 #sequence_revision Ol-Sep-1995 #text_change 13-Aug-1999
()Accession: S55395
R:Vitadello, M.; Vettore, S.; Lamar, E.; Chien, K.R.; Gorza, L.
submitted to the EMBL Data Library, January 1995
A:Description: Neurofilament mRNA and protein are expressed in precursors of A:Reference number: S55395
A;Accession: S55395
A;Accession: S55395
A;Accession: S55395
A;Accession: S5644 <VIT>A:Molecule type: mRNA
A:Residues: 1-644 <VIT>A:Gross-references: EMBL:Z47378; NID:g854352; PIDN:CAA87454.1; PID:g854353
C;Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                                                                                                                                     probable RNA helicase YIR002c - yeast (Saccharomyces K;Alternate names: hypothetical protein YIB2c C;Species: Saccharomyces cerevisiae C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #t C;Accession: S48436; S50885 R;Badcock, K.; Churcher, C. submitted to the EMBL Data Library, August 1994 A;Reference number: S48432 A;Accession: S48436
                                                                                                                                                                                                                         A;Cross-references: GB:Z47047; EMBL:Z38062; NID:g603997; PID:g763347; MIPS:YIR002c R;Voss, H.; Tamamos, J.; Teodoru, C.; Valencia, A.; Sensen, C.; Wiemann, S.; Schwag Yeast 11, 61-78, 1995
A;Title: Nucleotide sequence and analysis of the centromeric region of yeast chrome A;Reference number: S50795; MUID:95282515
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S48436
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A; Residues: 1-993 <BAD>
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Best Local Similarity
Matches 43; Conserv
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   RESULT 9
$73653
Nypothetical protein PO2_orf253 - My
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revis:
C;Accession: $73663
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A; Gene: ATSP:T15N24.80
A; Map position: 4
A; Introns: 345/3; 357/1
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL078465; GSPDB:GN00062; ATSP:T15N24.80 A;Experimental source: cultivar Columbia; BAC clone T15N24 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bevan, M.; Zimmermann, W.; Grueneisen, A.;
submitted to the Protein Sequence Database,
A;Reference number: 216518
A;Accession: T08929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-763 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;205-210/Region: nucleotide-binding F;209-212/Region: DEAD/H motif
                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 NEKTGVWEKRKIFVAT
                                 183 TCDDYNEKTGVWEKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 23.0 tes 45; Conservative
                                                                                                                                                                IPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQNISIAGHTFIDRPNYQFTN 132
NGDENKQVENVEGKEK
                                                                                                                                            DEDADGKK-----EQTDDGVSVEDTVMKENVESKDN--
                                                                                                                                                                                                                                                   AKPHIDNYLHD----KDKDEKIEQYDKNVKEQASKD----KKQQAKPQIPKDKSKVAGYIE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMGKTFIASTVMLNYFRWTKKAKIIFTAPTRPLVAQQIKACLGITGIPSDQTAILLDKSR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQKTVYEEIQRDVSFGPTHHELDYDALSFYVYPTNYEVRDYQYTIVHKSLFQNTLCAIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDYFSDFEDDELDKLYEKAINKSVKETITRRA----VPVQK--
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                                                                       EKETKETDITEADHKKAGKEDIQHEADKANGTKDGNTGDIKEEGTLVDEDKGTDMDEKVE
                                                                                                      LKAAKKGSMV---YFKVGNETRKYKMTSIRDVKPTDVG-----VLDEQKGKDKQLTLI 182
                                                                                                                                                                                                                 AEP--DNMEIDAQIKKDDEKAETEDKESEVKKNEDNAETQKMEEKVEVTKDEGQAEATNM 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPATP-EQLNRGVSFAEENESLDDQNISIAGH-TFIDRPNYQFTNL-KAAKKGSMVYFKV 146
                                                                                                                                                                                                                                                                                                                                                                                345/3; 357/1;
                                                                                                                                                                                                                                                                                        48;
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                                                                                                                                                                                                                                                                                      Conservative
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23.0%;
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 217
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                                                                                                                                                                                                                                                                                  27; Mismatches
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Pred. No. 12;
31; Mismatches
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Pred. No. 1
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May 1999
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                                                                                                                                          -NYAKDD 141
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#sequence_revision

25-Apr-1997 #text_change 07-Dec-1999

Mycoplasma

pneumoniae (strain

ATCC

29342)

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R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analyse of the genome of the A;Reference number: 87327; MUID:97105885
A;Accession: 873663
A;Status: preliminary; nucleic acid sequence not shown;
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C;Superfamily: hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AE000032; GB:U00089; A;Note: the nucleotide sequence was submitted C;Genetics:
                                                                                                                                                                                                                                                                                               A; Map position: 4
A; Introns: 41/1; 226/3
                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U88172; PIDN:AAB42258.1; GSPDB:GN00022; CESP:ZK354.3 A;Experimental source: strain Bristol N2; clone ZK354
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-312 < JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, February 1997 A;Description: The sequence of C. elegans cosmid A;Reference number: Z20120
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A; Residues: 1-253 <HIM>
                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: ZK354.3
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Johnson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T25994
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mes 48; Conserv
                                                                                                                                                                      30 DNYLHDK---DKDEKIEQYDKNVKEQASKDKKQQ--AKPQIPKDKSKVAGYIEIPDADIK 84
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                                                                                                                                                                                                            Local Similarity es 37; Conserv
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                                                                       DALVENPIVTEMSDRD----EKKEEKKD------
                                                                                                                                          DEKMDDKKPGEKEEKKEEFKKEMKKEEKKEEEKKEEPKKNDAPKKEGETKGEVK-----K
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                                   KVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRK 198
                                                                                                      EPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYF
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EEKKEEKKEEKKEE--KKDDKKEDDKEKSATKSEDKKSDEKKTEEKK
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21.3%;
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                                                                                                                                                                                                          Score 91.5; D
Pred. No. 5;
B5; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-17,19-21, 'p',23-204,'L',206-500,'E',501-845 <KEL>
A; Residues: 1-17,19-21, 'p',23-204,'L',206-500,'E',501-845 <KEL>
A; Cross-references: EMBL:212152; NID:956751; PIDN:CAA78136.1; PI
R; Xu, Z.S.; Liu, W.S.; Willard, M.B.
J. Biol. Chem. 267, 4467-4471, 1992
A; Title: Identification of strophorylation sites in the COOI
A; Reference number: A42393; MUID:92165797
A; Accession: A42393
                                                                                                                                                                                                                                                                                                          R;Kelly, B.M.; Gillespie, C.S.; Sherman, D.L. J. Cell Biol. 118, 397-410, 1992 A;Title: Schwann cells of the myelin-forming A;Reference number: S25712; MUID:92332596 A;Accession: S25712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_cha
C;Accession: A45669; S25712; A42393
R;Napolitano, E.W.; Chin, S.S.M.; Colman, D.R.; Liem, R.K.H.
J. Neurosci. 7, 2590-2599, 1987
A; Molecule type: nucleic acid
A; Residues: 411-500, 'E', 501-843, 'D'
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-845 < NAP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete amino acid sequence and A;Reference number: A45669; MUID:87282618 A;Accession: A45669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence A;Molecule type: DNA
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A; Title: Complete sequence analysis of the genome
A; Reference number: S73327; MUID:97105885
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C;Accession: S73333
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                                                  A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:M18628; NID:g205687; PIDN:AAA41696.1; R;Kelly, B.M.; Gillespie, C.S.; Sherman, D.L.; Brophy, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurofilament triplet M protein - rat
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submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23036
A; Accession: T46486
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1288 <AAA>
A; Cross-references: EMBL.AL136877
A; Experimental source: adult testis; clone DKFZp434F205
C; Genetics:
A; Note: DKFZp434F205.1
C; Superfamily: chromosome segregation protein SMC1
 hypothetical protein yhcS - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999 C;Accession: G69823 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosomal protein CAPC homolog DKFZp434F205.1 [similarity] - human c;Specles: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Jun-2000 C;Accession: T46486 R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Weil, B.; Wiemann, S.
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                                                                                                                                                                                                                                                                                 -FIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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Pred. No. 29;
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Albertini, A.M.; Alloni,
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 G.; Azevedo,
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A., Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquchi, J.; Sekowska A.; Sakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A.; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-1290 <HIR>
A;Residues: 1-1290 <HIR>
A;Cross-references: GB:Ul3673; NID:g563811; PIDN:AAA64679.1; PID:g563812
C;Superfamily: chromosome segregation protein SMC1
C;Keywords: chromosomal protein; DNA condensation; heterodimer
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
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A;Experimental source: strain 168
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A; Residues: 1-198 <KUN>
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                                                                                                                                                                                                        Query Match
320 YIHDLQKRSRDKEAQKEKIQEDTKDISEKSNTLLETMKEKNKALKDVEKQLNKITKFIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 TLQHEK---EELILTTCYPFS-YVGNAPKRYIIYGKRV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 VLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEV
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Local Similarity 23.4%;
                                                            32 YLHD-----KDKD---EKIEQYDKNVKEQA-----SKDKKQQAKPQIPKDKSKVAGYIE- 77
                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GTKNSTDQAKNKASFKPETGQASGILEIPKINAELPIVEG-TDADDLEKGVGHYKDSYYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDQ-NISIAGHTFIDRPNYQFTNLKAAKKGSM--VYFKVGNETRKYKMTSIRDVKPTDVG 167
                                                                                                                                        36; Conser
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Pred. No. 31;
13; Mismatches
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                                                                                                                                                                                                     Length 1290
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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     SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:6: sp_mammal:*
7: sp_mhc:*
8: sp_organelia:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr:
13: sp_vertebr:
14: sp_unclass:
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Gapop 10.0 , Gapext 0.5
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1076
1 MKKWTNRLMTIAGVVLILVA.....YNEKTGVWEKRKIFVATEVK 206
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                                                                                      sp_mammal:*
sp_mhc:*
sp_organelle:*
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sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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19	18	17	16	15	14	13	12	11	10	9	8	7	6	· UT	4	w	2	1	Result No.
91.5	91.5	92	93	93.5	94	96.5	97	97.5	97.5	101	102	104	106.5	126	133.5	182.5	184	1076	Score
8.5	8.5	8.6	8.6	8.7	8.7	9.0	9.0	9.1	9.1	9.4	9.5	9.7	9.9	11.7	12.4	17.0	17.1	100.0	Query
485	312	2268	253	763	643	1147	887	810	673	1017	552	352	231	365	194	187	193	206	Length
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P75139 mycoplasma	P91570 caen	Q93515 caen	P 7 5281 myco	Q9sual ara	Q9u229 caen	Q9y1h3 dict	Q06106 sacc	077788 bos	Q9u0n1 plas	Q9ss68 ara	P91122 caen	Q9xa14 stre	O31340 baci	068213 acti	Q9kb09 baci	Q9kfv9 baci	Q9kbb3 baci	Q9s446 stap	Description
plasma	caenorhabdi	caenorhabdi	mycoplasma	arabidopsis	caenorhabdi	dictyosteli	:haromyc	bos taurus	mod i.um	arabidopsis	caenorhabdi	streptomyce	bacillus ce	actinomyces	bacillus ha	bacillus ha	bacillus ha	staphylococ	

45	44					39																			
87.5	87.5	88	88	88.5	88.5	88.5	88.5	89	89	89	89	89	89	89	89	89.5	89.5	90	90	90.5	91	91.5	91.5	91.5	91.5
8.1	8.1	8.2	8.2	8.2	8.2	8.2	8.2	8. ₃	8.3	8 . 3	8 . 3	8.3	8 3	8 .ω	8 . 3	8.3	8.3	8.4	8.4	8.4	8 5	8 5	8 5	8 5	& .5
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Q9L5X4	Q9RPEO	Q9XV10	032032	096154	Q9U6W5	P72538	Q9R6P5	P91257	Q9UFR9	075032	044741	Q65023	Q9ZMK8	085224	Q39448	Q9Z6U5	Q9RB58	096127	Q9UEQ7	Q9K5S8	P93826	Q9NTJ3	095752	Q9UNT9	Q63370
Q915x4 streptococc		Q9xv10 caenorhabdi	O32032 bacillus su		Q9u6w5 caenorhabdi		Q9r6p5 streptococc			075032 homo sapien	044741 caenorhabdi	Q65023 aleutian mi	Q9zmk8 helicobacte	085224 helicobacte	Q39448 cicer ariet	Q9z6u5 chlamydia p	Q9rb58 chlamydia p	096127 plasmodium	Q9ueq7 homo sapien	Q9k5s8 bacillus ha	o	Q9ntj3 homo sapien	095752 homo sapien	Q9unt9 homo sapien	Q63370 rattus norv

ALIGNMENTS

Qy	Db :	Qy	В	Qy	Db	Qy	Ma Ma	SQ	DR.	RL	RŢ	RT	RA	RX	ج د	R A	2 2	8	8	SO	G I	D R	<u> </u>	DT	AC	ĪD	098446	RESULT
181 LITCDDYNEKTGVWEKRKIFVATEVK 206		121 TFIDRPNYQFTNLKAAKKGSMYYFKYGNETRKYKMTSIRDVKPTDVGYLDEQKGKDKQLT 180	61 AKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGH 120	61 AKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGH 120	1 MKKWTNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQ 60	1 MKKWINRLMIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQ 60	Ouery Match 100.0%; Score 10/b; DB 2; Length 20b; Best Local Similarity 100.0%; Pred. No. 4.3e-76; Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps	SEQUENCE 206 AA; 23541 MW; DC3E65C51E145C7B CRC64;	EMBL; AF162687; AAD48437.1;	Science 285:760-763(1999).	cell wall.";		Mazmanian S.K., Liu G., Ton-That H., Schneewind O.:	MEDLINE=99357874; PubMed=10427003;		SECTION OF FROM N A	NCBL_Tax1D=1280;	Bacillus/Staphylococcus group; Staphylococcus.	Bacteria; Firmicutes; Bacillus/Clostridium group;	Staphylococcus aureus.	SRTA		<pre>01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)</pre>	01-MAY-2000 (TrEMBLrel. 13, Created)	Q9S446;	Q9S446 PRELIMINARY; PRT; 206 AA.	40	T.T.

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RESULT
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Matches 53; Conserv
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STRAIN-C-125 / JCM 9153;
STRAIN-C-125 / JCM 9153;
STRAIN-C-125 / JCM 9153;
STRAIN-C-126 / JCM 9153;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001508; BAB04081.1; -.

SEQUENCE 187 AA; 21119 MW; CC26403CD0D01456 CRC64;
                                                                                                                                                                                                                                      Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                       Q9KFV9;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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STRAINEC-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001514; BAB05734.1;
SEQUENCE 193 AA; 21835 MW; DDF2567769F0177D CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
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29.3%;
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28.7%;
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                                      Score 182.5; DB Pred. No. 5.7e-07
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No. 4.5e-07
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KB09;
01-OCT-2000
01-OCT-2000
                                                                                                                                                      068213;
068213;
     Actinomycetales;
NCBI_TaxID=1655;
[1]
                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
Bacteria; Firmicutes; Bacacillus/Staphylococcus
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (T: BH2127 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KB09
                                                                        Actinomyces naeslundii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH2127
                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                         183
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                                                                                                                                                                                                                                                                                                                                                       123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C 171
                                                                                                                                                                                                                                                                                     TCDDYNEKTGVWEKRKIEVATEV
                                                                                                                                                                                                                                                       TCDPVKDPT - - - - - HRLIVQAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.48;
1 Similarity 24.18;
49; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                  Firmicutes;
                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                     Actinomycineae;
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15,
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                                                                                                                                                                                                                                                         189
                                                                                                                                                                                                                                                                                         205
                                                                                                                                                                       PRT;
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[1]
SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAIN=L: Nakasone K., Takaki Y.;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AP001514; BAB05846.1; -.
EMBL; AP001514; BAB05846.1; -.
194 AA; 22006 MW; 145BD7A2BE66A7CB CRC64;
                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PUTATIVE FIMBRIA-ASSCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTITAVLFISFGLLFMFFPRLQTEYYSFYETRLIDSYEKINRELEAFSNEE---PHLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQ-IP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RGNRHFSRLPDVTIGDEVFLHTKEETFVYKVTDISIIEPTDVDILDDRDGK-HEITMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GRQFNRLDEVEVGDVITVTINNHMYRYTVYSITVVEPTNIDIL-QHDGTAPVLTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEEPHAIGVLEIEKISLKLPVLQG-VDQETLKVGAGHMIESSPIGEKGNAAIAAHRSRTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQ-NISIAGH---TF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLIT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFTTDELNAVLELEIPSIELKQKVL-SETTEENLKLALTQLKENQHPGEGNFAIAGHRGY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGHTFI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQAS--KDKKQQAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKTRKILGVMLLLTGLILVSIPLYYEWQHGREV-----RALEEALSLISDYEQVEGT
                       Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 133.5; DB 2;
Pred. No. 0.0037;
6; Mismatches 99;
Actinomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                        365
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                       Actinobacteridae;
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Actinomyces
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Best Local S
Matches 55
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Best Local
Matches 4
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01-JAN-1998
01-JAN-1998
01-JAN-1998
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EMBL; AF019629; AAC13546.1; BB17A6A0DA8D5410 CRC SEQUENCE 365 AA; 39425 MW; BB17A6A0DA8D5410 CRC
                                                                                                                                                                                                                                                                                                                                                                            Rishovd A.L.;
Submitted (SEP-1997) to t)
EMBL; Y10908; CAA71849.1;
NON_TER 231 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-ATCC 10987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 1
Kolstoe A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=ATCC 10987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Staphylococcus
NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAPA.
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALL-ASSOCIATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kolsto A.B., Okstad
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                                                                                                          ASKDK-KQQAKP-QIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESL
                                                                                                                                                                KKWYRYLIQLIVVALIVTSIPLNGLAETAPPFTPSPNSEQSPEVEKKEEKELPDPH-PDQ
                                                                                                                                                                                                         KKWTNRLMTIAGVVLILVAAYL-----FAKPHIDNYLHDKDKDEKIEQYDKNVKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSKDSSLQYANILKANNEGLMARLKIPSISLDLPVYHGTA-DDTLLKGLGHL-EGTSLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDQNISIAGHTFIDRPNYQF----TNL----KAAKKGSMVYFKVGNETRKYKMTSIR--
                                                                                  LKKDKTKAQASPTEIVEERTETEKVFDNNDGTYTKKVYTEP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRVEEGKD-LLTLVTC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDEQKGKDKQLTLITC
    EEVSPKL - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGEGTRSVITGHRGLAEAT-MFTNLDKVKTGDSLIVEVFGEVLTYRVTSTKVVEPEETEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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(TrEMBLrel. ()
(TrEMBLrel. ()
                                                                                                                                                                                                                                                                                                                                                        231 AA;
                                                                                                                                                                                                                                                9.9%;
ilarity 24.0%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
-VEAPNAKIVTENTTLEPEFEKTTQDGKYVQFKVKDHTIKYKLMSANGE
                                                                                                                                                                                                                                                                                                                                                    231
26221 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            O.A., Lindback T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   the
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05, Last sequence update)
05, Last annotation update)
PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                     33,
                                                                                                                                                                                                                                              Score 106.5; DB
Pred. No. 0.56;
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 126; DB
Pred. No. 0.03
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                        2EB59CF9C9BA5678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hegna
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                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ι.,
                                                                                                                                                                                                                                                     82;
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                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                                                                                        CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lagreid
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                                                                                                                                                                                                                                                                                            231;
                                                                                HIEKNGKL
                                                                                                                                                                                                                                                     59;
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                                                                                                                                                                                                                                                Gaps
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  167
                                                                                112
                                                                                                                       110
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RESULT P91122

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PRELIMINARY;

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01-MAY-1997 01-MAY-1997 01-NOV-1998 P91122 P91122;

C32E12.1

SIMILARITY

HUMAN

(TrEMBLrel. 03, Created)
(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
HUMAN TO LINE-1 REVERSE TRANSCRIPTASE HO

HOMOLOG

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                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL079308; CAB45217.1;
SEQUENCE 352 AA; 37819 MW; D182503F05F0077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
01-NOV-1999 INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                            Redenbach M., Kieser H.M., Der
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and
                                                                                                                                                                                                                                                                                                                                                                                                                    Bentley S.D., Parkhill J., Submitted (JUN-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A set of ordered cosmids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XA14
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCH69.20C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9XA14;
313 RYITLTTCTPEFTSKYRMIVWGK 335
                         177
                                                   255
                                                                                                     195
                                                                                                                                                        148 GYLMLLFVTYQLWWTNVRAH------AQANQAASNLQDDWANGKRS------PGSFEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
                                                                            124
                                                                                                                              73
                                                                                                                                                                               13 GYVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGEVKPSPVTAT
                KQLTLITC-DDYNEKTG--VWEK
                                                                                                    QGFALLHIPKLDVVVPIAEGISSKKVLDRGMVGHYAEDGLKTAMPDAKAGNFGLAGHRNT
                                                                                                                            AGY--IEIPDADIKEPVYPGPATPEQLNRGV--SFAEE--NESLDDQ---NISIAGHTFI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DVKPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVK
                                                HGEPFRYIN--KLEPGDPIVVETQDKYFVYKMASILPVTSPSNVSVLDPVPKQSGFKGPG
                                                                          DRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDV-KPTDVGVLDEQ-----KGKD
                                                                                                                                                                                                           l Similarity
47; Conserv
                                                                                                                                                                                                           Conservative
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ptomycineae; Streptomycetaceae;
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           40;
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                                                                                                                                                                                                          Score 104; DB Pred. No. 1.5; 40; Mismatches
                         196
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                                                                                                                                                                                                           82;
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RESULT
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Best Local S
Matches 50
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston I
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of Contiguous nucleotide sequence from chromosome III of
elegans.";
                            PUTATIVE | T12J13.4.
                                                   Q9SS68;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U80034; FALLE STATE OF THE RNA-directed DNA polymerase. SPOUENCE 552 AA; 62427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston
Submitted
  Arabidopsis thaliana (Mou
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                     89SS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilcox L.;
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Eukaryota; Metazoa;
Rhabditidae; Pelode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                    KKPKDKKSKEKKPKAAKSKEVKSKDVKPKDVKSKDEKKKKKNSKGKKPSTDPLFSGPLTQ
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                                                                                                                                                                                                                                                                                                                    ASKHYKNKKDKKDKKDKKYKKYEQKDKKDKKEKNYKKGSKSDPNAVAKIKKNKKDKKSKD
                                                                                                                                                                                                                                                                                                                                         AKPHIDNYLHDKDKDE----KIEQYD-----KNVKEQASKD-
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                                          PHOSPHORIBOSYLANTHRANILATE
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                                                                                                       PRELIMINARY;
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.azoa; Nematoda; Chromadorea;
^^1^derinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                   9.5%;
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               (Mouse-ear cress)
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3, Last sequence update)
4, Last annotation update)
4, Last annotation update)
  Embryophyta;
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  Tracheophyta;
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  Spermatophyta;
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Best Local
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Best Local
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01-MAY-2000
01-MAY-2000
01-MAY-2000
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[1]
SEQUENCE FROM N.A
                                                                                                                                            Barrell B:
Submitted (SEP-1998) to the ENEL; AL031746: CAB63561.1; -
SEQUENCE 673 AA; 79795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnst Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome III BAC T12J13 genomic Submitted (CCT-1999) to the EMBL/GenBanK/DDBJ databases. EMBL; AC009327; AAF03465.1; -. INTERPRO; IPR000008; -.
                                                                                                                                                                                                                                  Plasmodium falciparum Eukaryota; Alveolata; NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                        Q9U0N1
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SEQUENCE 1
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                                                                                                                                                                                         Bowman S.,
                                                                                                                                                                                                    STRAIN=3D7;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        GARP
                                                                                                                                                                                                                                                                                 HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00168; C2;
181
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                                                      HDKDKDEKIEQYDKNVKEQASKDKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPAT
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                      PEQLNRGVSFAEEN ---
                                          HKKDKKEKKEKKDKKEKKD-KKEKKHKKEKKHKKDKKKE-----ENSEVMSLYKTGQHK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEKKEGDKKEEEKPKEEAKPDEK---KPDAPPDTKAKKPDTAVAPPPPPAEVKNPPIPQK 233
                                                                                       l Similarity
42; Conserv
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·NATEHGEENLYEEMVSEINNNAQGGLLLSSP-YQYREQGGCGIISSVH-ETSNDT
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                                                                                                                                                                                        Churcher
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) (TrEMBLrel. 13,
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24.1%;
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                     ESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNET 150
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                                                                                                                                                                                        Harris B.,
                                                                                      32;
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                                                                                      Score 97.5; D
Pred. No. 10;
32; Mismatches
                                                                                                                                                                                                                                                                                          Last
Last
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annotation
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10;
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                                                                                                                                                                                        Quail
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Е.,
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                                                                                     Gaps
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Qy
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Best Local S
Matches 41
                                                                                                                              006106 PRELIMINARY;

006106;

01-NOV-1996 (TrEMBLrel. 01,

01-NOV-1996 (TrEMBLrel. 11,

01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The bovine neurofilament M subunit has a novel set of K normally restricted to NF-H.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO ALL OTHER INTERMEDIATE FILAMENT PROTE EMBL; AF091342; AAC36357.1; -.
INTERPRO; IPR001664; -.
PFAM; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         077788
077788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
  Submitted (JUL-1995) to [2]
                        Nelson
                                 SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                            Saccharomycetaceae;
                                                                                      Eukaryota; Fungi; Ascomycota;
                                                                                                Saccharomyces cerevisiae (Baker's yeast)
                                                                                                             P8283.19
                                                                                                                       HYPOTHETICAL 101.1
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hill W.D., Zhang L., Balin B.J., Sprinkle
Gearhart D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TremBLrel.
01-MAY-2000 (TremBLrel.
NEUROFILAMENT-M SUBUNIT
                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               644
                                                                                                                                                                                                                                                                                                                                                                                                                                               intermediate filament; Coiled
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                                                                                                                                                                                                                                                                                                                                             KPHIDNYLHDKDKDEKIEQYDKNVKEQASKDK--KQQAKPQIPKDKSKVAGYIEIPDADI
                                                                                                                                                                                                                                                        DRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDK 177
                                                                                                                                                                                                                                                                            KEEVPAKPYKVSPEKEAKEEEKPQEKEKEKEKVEEVGGKEEGGLKESRKEDIAINGEV--
                                                                                                                                                                                                                                                                                                                         KPKAEAGAEKGEQKEKVEEEKKEAKESPKEEKAEKKEEKPKDVPEKKKAESPVK-AESPV
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                                                                                                                      KDA PROTEIN P8283.19
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                                                                          Saccharomyces
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Last annotation update)
            EMBL/GenBank/DDBJ
                                                                                                                                                        Created)
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                                                                                      Saccharomycetes;
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Best Local S
Matches 46
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Best Local S
Matches 35
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STRAIN-$288C / AB972;
Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U32445; AAB68082.1; -.
INTERPRO; IPRO00504; -.
PFAM; PF00076; rrm; 5.
PFONTE; PS00030; RNP_1; UNKNOWN_2.
                                                                                                                                                                                                                                                                 STRAIN-AX4; TRANSPOSON-RET Szafranski K., Gloeckner G Szafranski A., Winckler T.;
                                                                                                                                                                                     Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
EMBL; AF134171; AAD43059.1; -
INTERPRO; IPR000477; -
PFAM; PF00078; TYT; 1.
SEQUENCE 1147 AA; 134731 MW; D497537E1A024
                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold)
Eukaryota; Dictyosteliida; Dictyostel
                                                                                                                                                                                                                                                                                                                                                              POL.
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999
                                                                                                                                                                                                                                             "Non-LTR retrotransposons with unique integration preference downstream of Dictyostelium discoideum transfer RNA genes.";
                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000
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 333
                       112
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                  DQNISIAGHTFIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDE
                                                                                                            TNRLMTIAGVVLILVAAYLFAKPHIDN-YLHD----
 AWDIKLKLHLHQETPSKYLTSILKSRA---
                                          RDYLKKEQNKIKKEKNKRKYVIHKLLGNSDII-----
                                                     KD--KKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVS-FAEENESLD 111
                                                                                      TNRETTTTTTTKLERLPWTLCKEILNNKHIHDGLSELISKNKDKIKSVEEWTK-FKNNVI 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DRPNYQETNLKAAKKGSMVYFKVGNETR-----
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35; Conservative
                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                           TRANSPOSON=RETROTRANSPOSON TRE3-C;
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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134731 /
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22.2%;
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. 12, Last sequ
. 13, Last anno
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                                                                                                                                                                                                                                                                                                                                    Dictyostelium
                                                                                                                                   36;
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Pred. No. 16;
40; Mismatches
                                                                                                                                Score 96.5; I
Pred. No. 23;
86; Mismatches
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3 23;
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16;
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KDKSIFQIKDKDNKTISD
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                                                                                                                                                       Length 1147;
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                                          332
377
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Qy

172 QKGKDKQLTLITCDDYNEKTGVWEKRK 198

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RESULT
Q9U229
 RESULT 15
Q9SUA1
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Best Local Similarity 28.1%;
Matches 36; Conservative 1
Bevan
Mewes
                                                                                                Q9SUA1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 85.2 KDA PROTEIN.
T15N24.80 OR AT4G26630.
                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                           SEQUENCE FROM N.A.
                                                                                                                                                                              Q9SUA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology ";
Science 282:2012-2018(1998).
EMBL; AL132860; CAB60511.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
Y56A3A.32 PROTEIN.
                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00070; pyr_redox; 1.
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matthews
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR001100; INTERPRO; IPR001327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode
                                                                                                                                                                                                                                                            142 VYFKVGNE 149
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                                                                                                                                                                                                                                                                                                         93
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   H.W.,
                                                                                                                                                                                                                                                                                 KQAEQPEQAEEKQETKDAEPKEQVDDRQTEEAVHARRAPAAAEEP-----APSTSKADA
                                                                                                                                                                                                                                                                                                      ----TPEQL--NRGVSFAEENESLDDQNISIAGH-----TFIDRPNYQFTNLKAAKKGSM 141
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   Zimmermann
., Mayer K.F
                                                                                                                                                                                                                                                                                                                                                                                                                                 643 AA;
                                                                                                                                                                              PRELIMINARY;
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   K.F.X.,
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13,
  Grueneisen A.,
, Lemcke K., Sc
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                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                         Score 94; DB
Pred. No. 18;
12; Mismatches
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Search completed: March Job time: 90 sec

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                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AL078465; CAB43859.1; -. EMBL; AL161565; CAB79518.1; -. Hypothetical protein. SEQUENCE 763 AA; 85249 MW; D67F4F5BD4DB480
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                       TCDDYNEKTGVWEKRK 198
                                                 EKETKETDITEADHKKAGKEDIQHEADKANGTKDGNTGDIKEEGTLVDEDKGTDMDEKVE
                                                                          LKAAKKGSMV---YFKVGNETRKYKMTSIRDVKPTDVG-----VLDEQKGKDKQLTLI 182
                                                                                                                             IPDADIKEPVYPGPATPEQLNRGVS-----FAEENESLDDQNISIAGHTFIDRPNYQFTN 132
                                                                                                                                                                                 AKPHIDNYLHD----KDKDEKIEQYDKNVKEQASKD----KKQQAKPQIPKDKSKVAGYIE
                                                                                                                                                        AEP--DNMEIDAQIKKDDEKAETEDKESEVKKNEDNAETQKMEEKVEVTKDEGQAEATNM 104
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Pred. No. 24;
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*

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Copyright (c) 1993 - 2000 Compugen Ltd
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Sequence 3, Appli
Sequence 5465, Ap
Sequence 6656, Ap
Sequence 1023, Ap
Sequence 3336, Ap
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Sequence 4, Appli Sequence 488, App Sequence 37, Appl Sequence 37, Appl Sequence 300, Appl Sequence 34, Appli Sequence 7, Appli Sequence 23, Appli Sequence 23, Appli Sequence 2710, Ap Sequence 35, Appli Sequence 36, Appli Sequence 5, Appli Sequence 5, Appli Sequence 26, Appli Sequence 26, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 6184, Ap Sequence 6184, Ap Sequence 6714, Ap Sequence 6714, Ap Sequence 6714, Ap Sequence 67, Appli Sequence 6714, Ap Sequence 67, Appli Sequence 6714, Ap Sequence 67, Appli Sequence 67, Appli	equence 48 equence 59 equence 29 equence 29 equence 61 equence 61 equence 61

ALIGNMENTS

US-09-292-437-3

OY 1 MKKWINKLMIJAGVVLILVAAYLFAKDHIDNYLHDKDKDEKIEQYDKNYKEQASKDKKQQ 60	Query Match 100.0%; Score 1076; DB 27; Length 20 Best Local Similarity 100.0%; Pred. No. 3.1e-96; Matches 206; Conservative 0; Mismatches 0; Indels	; ORGANISM: Staphylococcus aureus US-09-292-437-3	; LENGTH: 206 . ; TYPE: PRT	; SEQ ID NO 3	; SOFTWARE: FastSEQ for Windows Version 3.0	; NUMBER OF SEQ ID NOS: 36	; CURRENT FILING DATE: 1999-04-15	; CURRENT APPLICATION NUMBER: US/09/292,437	; FILE REFERENCE: 510015.213	; TITLE OF INVENTION: IDENTIFICATION OF SORTASE GENE	; APPLICANT: Hung Ton-That	; APPLICANT: Gwen Liu	; APPLICANT: Sarkis Mazmanian	; APPLICANT: Olaf Schneewind	; GENERAL INFORMATION:	; Sequence 3, Application US/09292437
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                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                            Matches 204;
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                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/O FILING DATE: 01-APR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Karen J. TITLE OF INVENTION:
                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
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CITY: Kenilworth
STATE: New Jersey
                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 1...207
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 02-MAY-1996
APPLICATION NUMBER: 60/020,016
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/01 FILING DATE: 01-APR-1996 APPLICATION NUMBER: 60/01 FILING DATE: 02-MAY-1996
                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus aureus
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                                                            {\tt MKKWTNRLMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDNKQQ}
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George H. Miller
Roberta S. Hare
                                                                                                                            Conservative
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99.0%;
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Pred. No. 5.7e-95;
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                                    SEQ ID NO 6656
LENGTH: 207
TYPE: PRT
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PRIOR APPLICATION NUMBER: US (
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CURRENT FILING DATE: 2000-06-30
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ORGANISM: Staphylococcus aureus
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UMBER: US 09/036,082
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1998-03-06
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1999-03-11
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1997-04-01
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1998-03-06
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JMBER: US 09/037,934
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1998-03-06
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Sequence 3336, Application GENERAL INFORMATION:
APPLICANT: Haselbeck, R
APPLICANT: Ohlsen, KL
APPLICANT: Zyskind, JW
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Best Local Similarity
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APPLICANT: Ohlsen, K. L.
APPLICANT: Zyskind, J. W.
APPLICANT: Zyskind, J. W.
TITLE OF INVENTION: Genes Identified as essential
TITLE OF INVENTION: Staphylococcus aureus
FILE REFERENCE: ELITRA, 017PR2
CURRENT APPLICATION NUMBER: US/60/242,578
CURRENT FILING DATE: 2000-10-23
NUMBER OF SEG ID NOS: 1057
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TYPE: PRT
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Pred. No. 7.1e-95;
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Pred. No. 5
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US-09-450-969-4904
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Best Local S
Matches 148
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-09A
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SEQ ID NO 4904
LENGTH: 203
TYPE: PRT
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SOFTWARE: FastSEQ for
SEQ ID NO 3336
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Matches 204; Conserv
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APPLICANT: Wall, D
TITLE OF INVENTION: Genes identified as esse
TITLE OF INVENTION: typhimurium, Klebsiella
FILE REFERENCE: ELITRA.017PR4
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                                                                               TFIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLT 180
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                                                                                                                                                     AKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGH 120
                                                                                                                                                                                                             MKQWMNRLITLIGVLLIILAIYLFSKPYIDNYLHEKDNDHKIENYDKKEKEQT --- KTSK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVEVLDEQKGKDKQLT
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                                                         TFTDRSHYQFTNLKSAKIGSKVYFKTGNQTRKYKITKIRDVKPTEVKVLDEHPNKKNQLT
                                                                                                                                 STPKIPSDKSKMAGYIEVPDAQIKEPVYPGPATPEQLNRGVSFAEGDESLNQQNISIAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                     73.8%; Score 794.5; DB 18; ilarity 72.2%; Pred. No. 6.1e-69; Conservative 25; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes identified as essential in Staphylococcus aureus, typhimurium, Klebsiella pneumoniae and Pseudomonas aer
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99.0%;
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US-09-134-000-5985; Sequence 5985; Applices; GENERAL INFORMATION:
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; MOLECULE TYPE:
US-09-071-035-486
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: A Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
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                                                                                                                                 192 LIDDVPGQN-MITLITCGDLQATTRIAVQGTLAATTPIK 229
                                                                                                                                                    168 VLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVK 206
::|: |:: :|| || | : : : | :|
                                                                                                                                                                                                                                    108 ESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMYYFKVGNETRKYKMTSIRDVKPTDVG 167
                                                                                                                                                                                                     133 QVMGKNNYALASHRTEDGVSL-FSPLERTKKDELIYITDLSTVYTYKITSVEKIEPTRVE 191
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 52; Conserv
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                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                                                                                     14 KRGKNWLINSLLVLLFIIGLALIFNNQIRSWVVQQNSRSYAVSKLKPADVKKNMARETTF 73
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                                                   Application US/09134000A
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Pred. No. 2.5e-07
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RESULT 9
US-09-071-035-298
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; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000-5985
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CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 5985
LENGTH: 251
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Best Local
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INFORMATION FOR SEQ
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MOLECULE TYPE:
                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                  STRANDEDNESS:
                                                                                                                                                                               REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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CITY: Rockville
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52; Conserv
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23.7%;
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SEQ ID NO 29
LENGTH: 284
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Best Local S
Matches 56
     Sequence 29, Application US/60223804
GENERAL INFORMATION:
APPLICANT: Adderson, Elisabeth
APPLICANT: Bohnsack, John
TITLE OF INVENTION: GROUP B STREPT
TITLE OF INVENTION: THERAPEUTIC CO
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GENERAL INFORMATION:
APPLICANT: Adderson, Elisabeth
APPLICANT: Bohnsack, John
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/634,341
CURRENT FILING DATE: 2000-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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25.3%;
GROUP B STREPTOCOCCUS POYPEPTIDES NUCLEIC ACIDS THERAPEUTIC COMPOSITIONS AND VACCINES THEREOF
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US-09-292-437-6

Sequence 6, Application US/09292437

GENERAL INFORMATION:
APPLICANT: Olaf Schneewind
APPLICANT: Sarkis Mazmanian
APPLICANT: Gwen Liu
APPLICANT: Hung Ton-That
TITLE OF INVENTION: IDENTIFICATION OF SORTASE
FILE REFERENCE: 510015.213
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SOFTWARE: FastSEQ for
SEQ ID NO 6
LENGTH: 284
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/60/223,804
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 284
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Best Local Similarity
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Best Local
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CURRENT FILING DATE: 1999-04-15
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TYPE: PRT
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179 NGKTLAYQVDQIKTVEPTDTKDLHIESGQD-LVTLLTCTPY 218
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                                    GNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDY 187
                                                                          DKTNALLLEKGSSLLEGTSYPTGGTNTHAVISGHRGLPQAKL-FTDLPELKKGDEFYIEV 178
                                                                                                                                                       LQEKMEKKNQELAKKGSNPGLDPFSETQKTTKKPDKSYFESHTIGVLTIPKINVRLPIF - 119
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25.3%;
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Pred. No. 4.6e-07;
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Pred. No. 4.6e-07;
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 6125
LENGTH: 315
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000-6125
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US-09-107-532-5472
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US-09-134-000-6125
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Best Local S
Matches 56
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
                 APPLICATION NUMBER: 60/085
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0515
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                              SOFTWARE: CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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NAME:
                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
STATE: Massac
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nes 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKSKKKRRIIDGFMILLLIIGIGAFAYPFVSDALNNYLDQQIIAHYQAKASQENTKEMAE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPATPEQLNRGVSFAEENE----SLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKV 146
                                                                                                                                                                                                                                                                                                                                             02354
Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                             100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                   CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.7%; Score 158.5; DB 15; Length 315; 25.3%; Pred. No. 5.3e-07; tive 38; Mismatches 90; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7308
                                                                                                                            60/ 085598
                                                                                                                                                                                            US/09/107,532
                                                              60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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DЬ
                                  Qγ
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                                                                                                                                                                                                                                                     ; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-292-437-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-292-437-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-107-532-5472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09292437 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 4
                                                                                                                                                        Query Match
Best Local Similarity
Matches 47; Conserva
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gwen Liu
APPLICANT: Hung Ton-That,
APPLICANT: HUNG TON-That,
TITLE OF INVENTION: IDENTIFICATION OF SORT
FILE REFERENCE: 510015.213
CURRENT APPLICATION NUMBER: US/09/292,437
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: pro
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                    116 SIAG---HTFIDR----PNYQ-FTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VTYLEPNPNEDR-VTLMTCTPKGINTHRFLVYGKRVTFTKSELK 223
83 PVGGDGTHTVISAHRGLPSAEMFTNLNLVKKGDTFYFRVLNKVLAYKVDQILTVEPDQVT 142
                                                                           32
                                                                                               56 DKKQQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 TAAETDSSLDVAKIELGDPVGILTIPSISLKLPIYDG-TSDKILENGVGITEGTGDITGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 25.4 nes 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 1...259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKWTNR--LMTIAGVVLILVAAYLFAKPHIDNYLHDKDKDEKIEQYDKNVKEQASKDKK 58
                                                                         DKNYESLLQI--ENNDIMGYVEVPSIKVTLPIY-HYTTDEVLTKGAG------HLFGSAL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGVLDEQKGKDKQLTLITCDDYNEKTG---VWEKRKIFVATEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGKNPLIAGHSGLYKDNL-FDDLPSVKKGEKFYIKVDGEQHAYQIDRIEEVQKDELQRNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQAKPQIPKDKSKV-----AGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESL--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGKWIIAFWLLSAVGVLLLMPA--------EASVAKYQQNQQIAAIDRTG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sarkis Mazmanian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01af
                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION OF SORTASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%; Score 157.5; DB 25.4%; Pred. No. 5e-07;
                                                                                                                                                                      14.5%; Score 156; DB 27; 32.6%; Pred. No. 5.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5472:
                                                                                                                                                        19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 68
                                                                                                                                                        60;
                                                                                                                                                                                          Length 227;
                                                                                                                                                      Indels
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                                                                                                                                                      18;
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                                                                                                                                                      Gaps
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Search completed: March 2, 2001, 10:24:18 Job time: 125 sec

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